

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:43:51 ; Search time 166 Seconds
(without alignments)
866.716 Million cell updates/sec

Title: US-10-666-689-6

Perfect score: 1953

Sequence: 1 MNYPLTLEMDLENLEDFWE.....PSWRSSLSSENAISLTTF 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003s:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	372	2	AAR27793 New plate
2	1953	100.0	372	2	AAR68813 Human lym
3	1953	100.0	372	2	AAR92239 Chemokine
4	1953	100.0	372	2	AAY06644 Human Bur
5	1953	100.0	372	3	AAY06627 Human G p
6	1953	100.0	372	4	AAG80124 Human CX
7	1953	100.0	372	6	ABP81789 Human CX
8	1953	100.0	372	7	ADC22585 Human G p
9	1953	100.0	372	8	ADH14058 Human BLR
10	1953	100.0	372	8	ADJ45761 Human CX
11	1953	100.0	372	8	ADO29199 Human GPC
12	1953	100.0	372	8	ADRE6972 Human can
13	1953	100.0	378	4	ABB11873 Human Bur
14	1947	99.7	372	3	AAY90661 Human mut
15	1947	99.7	372	7	ADC22719 Human G p
16	1947	99.7	372	7	ADH14192 Mutated h
17	1638	83.9	374	8	ADRE6969 Mouse can
18	1635	83.7	374	8	AAY06643 Mouse Bur
19	1635	83.7	374	8	ADO29200 Mouse GPC
20	1470	75.3	741	4	ABG19581 Novel hum
21	635	32.5	368	2	AAY54371 Human IP-
22	635	32.5	368	3	AAY90614 Human G p
23	635	32.5	368	4	AAG80122 Human CX
24	635	32.5	368	6	ABP81795 Human CX
25	635	32.5	368	7	AAG38602 Human C-X

26	635	32.5	368	7	ADC22539	Adc22539 Human G p
27	635	32.5	368	7	ADF17988	Adf17988 Human CX
28	635	32.5	368	7	ADH14012	Adh14012 Human GPR
29	635	32.5	368	7	ADN39434	Adn39434 Cancer/an
30	635	32.5	368	8	ADH61810	Adh61810 Human G p
31	635	32.5	368	8	ADO29458	Ado29458 Human GPC
32	635	32.5	368	8	ADFI2496	Adfi2496 Protein e
33	635	32.5	368	8	ADFI2922	Adfi2922 Protein e
34	635	32.5	368	8	ADQ09119	Adq09119 Human CX
35	635	32.5	368	8	ADQ59336	Adq59336 T cell ac
36	635	32.5	368	8	ADR67008	Adr67008 Human can
37	635	32.5	368	8	ADS73812	Adse73812 Human CX
38	635	32.5	378	2	AAY50129	Aay50129 Human che
39	635	32.5	415	7	ADC46963	Adc46963 Human CX
40	635	32.5	415	8	ADH61808	Adh61808 Human G p
41	634	32.5	415	8	ADQ59388	Adq59388 T cell ac
42	632	32.4	368	3	AAY90648	Aay90648 Human mut
43	632	32.4	368	7	ADC22693	Adc22693 Human G p
44	632	32.4	368	7	ADH14166	Adh14166 Mutated h
45	630	32.3	368	8	ADS73816	Adse73816 Human non

ALIGNMENTS

RESULT 1
AAR27793
ID AAR27793 standard; protein; 372 AA.
XX
AC AAR27793;
XX
DT 25-MAR-2003 (revised)
DT 12-MAR-1993 (first entry)
XX
DE New platelet factor 4 receptor superfamily member PF4ARii.
XX
KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
KW pro-inflammatory cytokine; 8rr.9.
XX
OS Homo sapiens.
XX
FN WO9217497-A1.
XX
PD 15-OCT-1992.
XX
PF 23-MAR-1992; 92WO-US002317.
XX
PR 29-MAR-1991; 91US-00677211.
PR 19-DEC-1991; 91US-00810782.
XX
(GETH) GENENTECH INC.
XX
PI Lee J, Holmes WF, Wood WI;
XX
WPI; 1992-366191/44.
XX
N-PSDB; AAQ37107.
XX
Isolated human platelet factor 4 super-family receptor polypeptide and
corresp. antibodies and DNA - useful as diagnostic and screening agents,
and for treating inflammation or PF4AR-mediated disorders.
XX
Claim 7; Fig 5; 78pp; English.
XX
The IL-8 receptor cDNA sequence was isolated (see AAO29505) and a 874bp
sub-fragment of the coding sequence was used as a probe to screen human
cell line HL60 and human peripheral blood lymphocyte cDNA libraries. Two
new gene sequences were found that are clearly related to the IL-8
receptor. One of these was contained in clone 8rr.9 and is predicted to
encode an amino acid sequence which is 36% and 38% identical with the
high and low affinity IL-8 receptor sequences, respectively. See also
AAQ37107. (Updated on 25-MAR-2003 to correct FN field.)
XX
Sequence 372 AA;
SQ

Query Match 100.0%; Score 1953; DB 2; Length 372; Mismatches 0; Indels 0; Gaps 0;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
 DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVLILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWVLTGF 120
 DB 61 IFLLGVIGNVLVLILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180
 DB 121 LCKTVIALHKVNFYCSSLLACIAVDYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
 DB 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
 DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
 DB 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372

RESULT 2
 AAR68813
 ID AAR68813 standard; protein; 372 AA.
 AC AAR68813;
 XX
 XX 25-MAR-2003 (revised)
 DT 18-JUL-1995 (first entry)
 DE Human lymphocyte PF4AR.
 XX
 XX Interleukin-8 receptor; IL-8 receptor; PF4AR;
 KW platelet factor superfamily receptor; lymphocyte; chemotactic;
 KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
 KW fibrosis; colitis; bronchitis; meningitis; therapeutic.
 OS
 OS Homo sapiens.
 XX
 XX WO9428931-A1.
 PN
 XX
 XX 22-DEC-1994.
 XX
 XX 07-JUN-1994; 94WO-US006380.
 XX
 XX 11-JUN-1993; 93US-00076093.
 PR
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Chuntharapai A, Lee J, Hebert C, Kim KJ;
 PI
 XX WPI; 1995-036114/05.
 DR N-PSDB; AAQ80522.
 DR
 XX
 XX Treatment of inflammatory disorders - by administering an antibody
 PT capable of binding a platelet factor 4 superfamily receptor polypeptide.
 PT
 XX
 XX Disclosure; Page 56-58; 83pp; English.
 XX
 XX 2 PF4AR members were identified by probing lambda libraries from human

CC monoclyte-like cell line HL-60 and human peripheral blood lymphocytes
 CC using a large fragment of IL-8 receptor DNA (full sequence given in
 CC AAQ80520). The nucleotide sequences of the 2 PF4ARs are given in AAQ80521
 CC and AAQ80522, and their respective amino acid sequences in AAR68812 and
 CC AAR68813. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
 DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVLILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWVLTGF 120
 DB 61 IFLLGVIGNVLVLILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180
 DB 121 LCKTVIALHKVNFYCSSLLACIAVDYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
 DB 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
 DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
 DB 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372

RESULT 3
 AAR92239
 ID AAR92239 standard; protein; 372 AA.
 AC AAR92239;
 XX
 XX 25-MAR-2003 (revised)
 DT 26-MAR-1996 (first entry)
 DE Chemokine superfamily receptor.
 XX
 XX Interleukin; IL-8; inflammation; psoriasis; dermatitis;
 KW rheumatoid arthritis; inflammatory bowel disease;
 KW chronic lung inflammation; treatment; antibody; affinity purification;
 KW detection.
 OS
 OS Homo sapiens.
 XX
 XX US5440021-A.
 PN
 XX
 XX 08-AUG-1995.
 XX
 XX 25-FEB-1994; 94US-00202056.
 XX
 XX 29-MAR-1991; 91US-00677211.
 XX
 XX (HEBE/) HEBERT C.
 PA (CHUN/) CHUNTHARAPAI A.
 PA (KIMK/) KIM K J.
 PA (LEEJ/) LEE J.
 XX
 XX Chuntharapai A, Kim KJ, Hebert C, Lee J;

XX WPI; 1995-283151/37.
 DR N-PSDB; AAQ99009.
 XX
 PT New antibodies against interleukin 8 type B receptor - used to treat or
 PT prevent inflammation, also for detecting receptor expression and
 PT purificn.
 XX
 XX Example 2; Col 49-52; 62pp; English.
 XX
 XX Antibodies directed against the interleukin-8 receptor B can be used to
 CC treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid
 CC arthritis and particularly inflammatory bowel disease and chronic lung
 CC inflammation. When immobilised, these antibodies may be used to detect
 CC interleukin-8 receptor B expression in cells and tissues and for affinity
 CC purification of interleukin-8 receptor B from cells. This sequence is an
 CC additional chemokine superfamily receptor which was identified by probing
 CC lambda libraries of genomic DNA from a human monocyte-like cell line (L-
 CC 60) and human peripheral blood lymphocytes using a large fragment of the
 CC interleukin-8 type A receptor DNA (See AAQ99006). (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX
 XX Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLDFWELDRDLDNYNDTSLVENHLCPTGEGPLMASFKAVFVPVAYS 60
 RB 1 MNYPLTLEMDLENLDFWELDRDLDNYNDTSLVENHLCPTGEGPLMASFKAVFVPVAYS 60
 QY 61 IFLLGVIGNVLVILERHQRSSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
 DB 61 IFLLGVIGNVLVILERHQRSSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
 QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
 DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
 QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLPMLVMGCVY 240
 DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLPMLVMGCVY 240
 QY 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKL 300
 DB 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKL 300
 QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWR 360
 DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWR 360
 QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372

RESULT 4
 AA006644
 ID AA006644 standard; protein; 372 AA.
 XX
 AC AA006644;
 XX
 DT 26-OCT-1999 (first entry)
 XX
 DE Human Burkitt's lymphoma receptor 1 (BLR1).
 XX
 KW Burkitt's lymphoma receptor 1; BLR1; human; B lymphocyte chemoattractant;
 KW BLC; chemokine; ligand; drug screening; leukaemia; autoimmune disease;
 KW therapy.
 XX
 OS Homo sapiens.
 XX

PN WO9928468-A1.
 XX
 PD 10-JUN-1999.
 XX
 PF 02-DEC-1998; 98WO-US025561.
 XX
 XX 02-DEC-1997; 97US-00982493.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Gunn MD, Williams LT, Cyster JG;
 XX
 XX WPI; 1999-493764/41.
 DR N-PSDB; AA087710.
 XX
 PT Modulating interaction of a Burkitt's Lymphoma Receptor 1 polypeptide and
 PT ligand, useful in drug screens.
 XX
 XX Claim 1; Page 38; 42pp; English.

XX This sequence represents human Burkitt's lymphoma receptor 1 (BLR1). The
 CC invention relates to methods for modulating the interaction of BLR1 with
 CC its ligand. B lymphocyte chemoattractant (BLC, see AA006642). The methods
 CC comprise combining BLR1 and BLC polypeptides with a candidate modulator
 CC agent under conditions whereby, but for the presence of the agent, the
 CC polypeptides engage in a first interaction, and determining a second
 CC interaction of the polypeptides in the presence of the agent, wherein a
 CC difference between the first and second interactions indicates that the
 CC agent modulates the interaction of the polypeptides. The modulator is
 CC preferably an antagonist, especially dominant negative, form of BLC. BLC
 CC and BLC agonists and antagonists may be useful for treating viral (e.g.
 CC HIV) infections, lymphoma, B lineage leukaemia, and autoimmune diseases
 CC such as rheumatoid arthritis, thyroiditis and diabetes
 XX

SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLDFWELDRDLDNYNDTSLVENHLCPTGEGPLMASFKAVFVPVAYS 60
 DB 1 MNYPLTLEMDLENLDFWELDRDLDNYNDTSLVENHLCPTGEGPLMASFKAVFVPVAYS 60
 QY 61 IFLLGVIGNVLVILERHQRSSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
 DB 61 IFLLGVIGNVLVILERHQRSSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
 QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
 DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
 QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLPMLVMGCVY 240
 DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLPMLVMGCVY 240
 QY 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKL 300
 DB 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKL 300
 QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWR 360
 DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWR 360
 QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372

RESULT 5
 AA006627
 ID AA006627 standard; protein; 372 AA.
 XX

AC AAY90627;
 XX 21-AUG-2000 (first entry)
 XX Human G protein-coupled receptor BLR1.
 DE
 XX G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
 KW antagonist.
 XX
 XX Homo sapiens.
 OS
 XX W0200022129-A1.
 PN
 XX 20-APR-2000.
 XX
 XX 12-OCT-1999; 99WO-US023938.
 PF
 XX 13-OCT-1998; 98US-00170496.
 PR
 XX (AREN-) ARENA PHARM INC.
 PA
 XX Behan DP, Chalmers DT, Liaw CW;
 PI
 XX WPI; 2000-329165/28.
 DR
 DR N-PSDB; AAA30626.
 XX
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents.
 XX
 XX Example 1; Page 152-153; 341pp; English.
 PS
 XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
 CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
 CC and AAA30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
 CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present sequence
 CC represents a human wild-type GPCR referred to in an exemplification of
 CC the invention
 XX
 XX Sequence 372 AA;
 SQ
 Query Match 100.0%; Score 1953; DB 3; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
 DB 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
 QY 61 IFLGVIGNVLVILVILRRHQTRSSSTETFLFLAVADLLVFLIPFAVAGSGVWLGTF 120
 DB 61 IFLGVIGNVLVILVILRRHQTRSSSTETFLFLAVADLLVFLIPFAVAGSGVWLGTF 120
 QY 121 LCKTVIALHKVNFYCSSLLACIADVRYLAIHVHAYHRRLLSIHITCGTILWVGFL 180

DB 121 LCKTVIALHKVNFYCSSLLACIADVRYLAIHVHAYHRRLLSIHITCGTILWVGFL 180
 QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAMFTSRFLYHVAGFLPMLVMGWCYVG 240
 DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAMFTSRFLYHVAGFLPMLVMGWCYVG 240
 QY 241 VVHRLRQARRPQROKAVRVAILVTSIFPLCWSPHIVIFLDTLRLKAVDNTCKLNGSL 300
 DB 241 VVHRLRQARRPQROKAVRVAILVTSIFPLCWSPHIVIFLDTLRLKAVDNTCKLNGSL 300
 QY 301 PVAITMCBFLGLAHCLNPLMTYFAGVKFRSDLSRLTLKLGCTGPASLCQLPSPWRRSSL 360
 DB 301 PVAITMCBFLGLAHCLNPLMTYFAGVKFRSDLSRLTLKLGCTGPASLCQLPSPWRRSSL 360
 QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372
 RESULT 6
 AAG80124
 ID AAG80124 standard; protein; 372 AA.
 XX
 AC AAG80124;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CXCR5 protein.
 XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX
 XX Homo sapiens.
 OS
 PN W0200172830-A2.
 PD 04-OCT-2001.
 XX
 PF 02-APR-2001; 2001WO-EP003708.
 PR 31-MAR-2000; 2000DE-01016013.
 XX (IPFP-) IPF PHARM GMBH.
 PA (FORS-) FORSSMANN U.
 PA
 PI Forssmann W, Adermann K, Heitland A, Spodeberg N;
 XX WPI; 2001-626256/72.
 DR
 PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX
 PS Disclosure; Page 12-13; 26pp; German.
 XX
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine

CC fragments used to illustrate the method of the invention
XX
SQ Sequence 372 AA;

Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYSL 60

QY 61 IFLLGVIGNVLVLILRHRQTRSTETFLFHLAVADLLVFLPFAVAEGSVGWLTGF 120
DB 61 IFLLGVIGNVLVLILRHRQTRSTETFLFHLAVADLLVFLPFAVAEGSVGWLTGF 120

QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAVHAYRHRLLSHITCGTILWVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAVHAYRHRLLSHITCGTILWVGFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENOAETHAWFTSRFLYHVAGFLPMLVMGVCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENOAETHAWFTSRFLYHVAGFLPMLVMGVCYVG 240

QY 241 VVHRLQAQRPRQOKAVRAILVTSIFFLCNSPYHIVIFDLTARLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQOKAVRAILVTSIFFLCNSPYHIVIFDLTARLKAVDNTCKLNGSL 300

QY 301 PVAITWCEFLGLAHCCNLMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITWCEFLGLAHCCNLMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 10
ADJ45761
ID ADJ45761 standard; protein; 372 AA.
XX AC ADJ45761;
XX XX
DT 06-MAY-2004 (first entry)
XX DE Human CXCR5 receptor, seq id 2.
XX KW Cardiovascular; cytostatic; respiratory; CNS; central nervous system; gene therapy; hematological disease; cancer; cardiovascular disease; respiratory disease; CXCR5 chemokine receptor 5; CXCR5, human.
XX OS Homo sapiens.
XX PN WO2004015426-A1.
XX PD 19-FEB-2004.
XX PF 24-JUL-2003; 2003WO-EP008141.
XX PR 06-AUG-2002; 2002EP-00017628.
XX PA (FARB) BAYER HEALTHCARE AG.
XX PI Golz S, Brueggemeier U, Summer H;
XX DR WPI; 2004-191806/18.
XX DR N-PSDB; ADJ45760.
XX PT Screening for therapeutic agents, useful in diagnosing or treating hematological or cardiovascular diseases and cancer, comprises contacting a test compound with a CXCR5 chemokine receptor 5 and determining activity.
XX PS Disclosure; SEQ ID NO 2; 131pp; English.
XX XX
XX CC The invention relates to a method for screening for therapeutic agents useful in the treatment of hematological diseases, cancer, cardiovascular diseases, respiratory diseases and disorders of the peripheral and central nervous system in a mammal. The method of the

CC invention comprises contacting a test compound with a CXCR5 chemokine receptor 5 (CXCR5) polypeptide or polynucleotide. The method of the invention is useful in screening for therapeutic agents that may be useful in treating the diseases mentioned above. The regulators of a CXCR5 are useful for regulating CXCR5 activity or for preparing a pharmaceutical composition for the treatment of the stated diseases in a mammal. The method and compositions are also useful in diagnosing and treating the stated diseases. The current sequence represents the human CXCR5 receptor.
XX CC
XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 8; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYSL 60

QY 61 IFLLGVIGNVLVLILRHRQTRSTETFLFHLAVADLLVFLPFAVAEGSVGWLTGF 120
DB 61 IFLLGVIGNVLVLILRHRQTRSTETFLFHLAVADLLVFLPFAVAEGSVGWLTGF 120

QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAVHAYRHRLLSHITCGTILWVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAVHAYRHRLLSHITCGTILWVGFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENOAETHAWFTSRFLYHVAGFLPMLVMGVCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENOAETHAWFTSRFLYHVAGFLPMLVMGVCYVG 240

QY 241 VVHRLQAQRPRQOKAVRAILVTSIFFLCNSPYHIVIFDLTARLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQOKAVRAILVTSIFFLCNSPYHIVIFDLTARLKAVDNTCKLNGSL 300

QY 301 PVAITWCEFLGLAHCCNLMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITWCEFLGLAHCCNLMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 11
ADO29199
ID ADO29199 standard; protein; 372 AA.
XX AC ADO29199;
XX DT 29-JUL-2004 (first entry)
XX DE Human GPCR BLR1, SEQ ID NO:300.
XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianxiety; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic; dermatological; antitumor; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; receptor.
XX OS Homo sapiens.
XX XX

PN WO2004040000-A2.
 XX 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilakis D, Zeng H;
 XX
 DR WPI; 2004-390329/36.
 DR N-PSDB; ADO29818.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 300; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 372 AA;
 Query Match 100.0%; Score 1953; DB 8; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
 DB 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
 QY 61 IFLGVIGNVLVLILERHQRTRSTETFLFLHVLADLLVFLPFAVAGSVGVWLGTG 120
 DB 61 IFLGVIGNVLVLILERHQRTRSTETFLFLHVLADLLVFLPFAVAGSVGVWLGTG 120
 QY 121 LCKTVIALHKVNFYCSSLLACIAVDRLYLAIVHAYHRRRLLSIHITCGTIWLGVFL 180
 DB 121 LCKTVIALHKVNFYCSSLLACIAVDRLYLAIVHAYHRRRLLSIHITCGTIWLGVFL 180

QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRPLHYHAGFLPLMLVMGWCYVG 240
 DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRPLHYHAGFLPLMLVMGWCYVG 240
 QY 241 VVHRLRQARRRQOROKAVRAVAILVTISIFFLCKSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
 DB 241 VVHRLRQARRRQOROKAVRAVAILVTISIFFLCKSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
 QY 301 PVAITMCEFLGLAHCCNPNMPLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLPFSWRSSSL 360
 DB 301 PVAITMCEFLGLAHCCNPNMPLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLPFSWRSSSL 360
 QY 361 SESENATSLTTP 372
 DB 361 SESENATSLTTP 372
 RESULT 12
 ADR66972
 ID ADR66972 standard; protein; 372 AA.
 XX
 AC ADR66972;
 XX
 DT 18-NOV-2004 (first entry)
 DE Human cancer associated protein sequence SEQ ID NO:18.
 DE
 XX
 KW cancer; cancer associated nucleic acid; cancer associated gene;
 KW cancer associated protein; CAP; cytostatic; vaccine; gene therapy;
 XX lymphoma; leukaemia; human.
 OS Homo sapiens.
 XX
 PN WO2004074321-A2.
 XX
 PD 02-SEP-2004.
 PF 17-FEB-2004; 2004WO-US005000.
 PF
 XX 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 23-SEP-2003; 2003US-00669920.
 PR 15-DEC-2003; 2003US-00737318.
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX Morris DW, Malandro MS;
 PI
 XX WPI; 2004-652915/63.
 DR N-PSDB; ADR66970, ADR66971.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS Claim 18; SEQ ID NO 18; 166pp; English.
 XX
 CC The present invention describes an isolated cancer associated (CA)
 CC nucleic acid (1). Also described: (1) an expression vector comprising (1)
 CC ; (2) a host cell comprising (1) or the expression vector; (3) a
 CC microarray for detecting a CA nucleic acid; (4) an isolated cancer
 CC associated protein (CAP) polypeptide, encoded within an open reading
 CC frame of a CA sequence; (5) an isolated antibody, or its antigen binding
 CC fragment, that binds to the above polypeptide; (6) a hybridoma that
 CC produces the above monoclonal antibody; (7) a pharmaceutical composition
 CC comprising the above antibody and a pharmaceutical excipient; (8) a kit
 CC for detecting cancer cells, comprising the monoclonal antibody
 CC described above; (9) methods for diagnosing cancer or for detecting the
 CC presence or absence of cancer cells in an individual; (10) a method for
 CC inhibiting growth of cancer cells in an individual; (11) a method for
 CC delivering a therapeutic agent to cancer cells in an individual; (12) an
 CC electronic library comprising the above polynucleotide or polypeptide, or

CC their fragments; (13) methods of screening for anticancer activity or for
CC a bioactive agent capable of modulating the activity of a CAP; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC in a test cell sample, or with the presence of an antibody in a test
CC serum sample; (15) a method for treating cancers; and (16) a method for
CC inhibiting the expression of CA gene in a cell. The CA sequences have
CC cytotatic activity, and can be used in vaccines, and in gene therapy.
CC The composition and methods are useful for detecting, diagnosing,
CC preventing and treating cancers, especially lymphoma and leukaemia. They
CC may also be used in screening for agents that modulate cancer. The
CC present sequence represents a cancer associated protein (CAP) sequence,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 8; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGELMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGELMASFKAVFPVAYSL 60
QY 61 IFLLGVIGNVLVILERHROTSTRSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120
DB 61 IFLLGVIGNVLVILERHROTSTRSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120
QY 121 LCKTVIALHKVNFYCSLLACIADRYLAIVHAVHAYRHRLLSHITCGTILWVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIADRYLAIVHAVHAYRHRLLSHITCGTILWVGFL 180
QY 181 ALPEILFAKVSQGHNNLSPRCTFSQENQAEHTAFTSRPLXHVAGFLPMLVNGCYVG 240
DB 181 ALPEILFAKVSQGHNNLSPRCTFSQENQAEHTAFTSRPLXHVAGFLPMLVNGCYVG 240
QY 241 VVHLRQAQRPRQKAVRAVAILVTSIFFLCWSPYHIVFLDTLARKAVDNTCKLNGSL 300
DB 241 VVHLRQAQRPRQKAVRAVAILVTSIFFLCWSPYHIVFLDTLARKAVDNTCKLNGSL 300
QY 301 PVAITWCEFLGLAHCLNPMFLYFAGVKFRSLRLTLKLGCTGPASLQOLFSPWRRSSL 360
DB 301 PVAITWCEFLGLAHCLNPMFLYFAGVKFRSLRLTLKLGCTGPASLQOLFSPWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 13
ABB11873
ID ABB11873 standard; peptide; 378 AA.

AC ABB11873;

XX 11-JAN-2002 (first entry)

XX Human Burkitt lymphoma receptor homologue, SEQ ID NO:2243.

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytotatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX Homo sapiens.

XX WO200157188-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US003800.
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457740/49.
XX N-PSDB; ABA09117.
XX Human proteins and DNA encoding sequences useful for preventing, treating
XX or ameliorating a medical condition in a mammalian subject e.g. arthritis
XX and cancer.
XX Claim 20; Page 269; 1963pp; English.

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention

SQ Sequence 378 AA;

Query Match 100.0%; Score 1953; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGELMASFKAVFPVAYSL 60
DB 7 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGELMASFKAVFPVAYSL 66
QY 61 IFLLGVIGNVLVILERHROTSTRSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120

Db 67 IFLLGVIGNVLVLVILSRHQTRSTETFLFHLAVADLLLVILPFAVAGSVGVVLGTF 126
Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHYRHRLLSIHITCGTIWLVGFL 180
Db 127 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHYRHRLLSIHITCGTIWLVGFL 186
Qy 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
Db 187 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 246
Qy 241 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 247 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVDNTCKLNGSL 306
Qy 301 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
Db 307 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 366
Qy 361 SESENATSLTTF 372
Db 367 SESENATSLTTF 378

RESULT 14

AA90661
ID AAY90661 standard; protein; 372 AA.
XX AC AAY90661;
XX DT 21-AUG-2000 (first entry)
XX DE Human mutant G protein-coupled receptor BUR1 (V258K).
XX KW G protein-coupled receptor; GPCR; constitutively active;
XX KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
XX KW antagonist; mutant; mutein.
XX QS Homo sapiens.
XX OS Synthetic.
XX PN W0200022129-A1.
XX PD 20-APR-2000.
XX PF 12-OCT-1999; 99WO-US023938.
XX PR 13-OCT-1998; 98US-00170496.
XX PA (AREN-) ARENA PHARM INC.
XX PI Behan DP, Chalmers DT, Liaw CW;
XX DR WPI; 2000-329165/28.
XX DR N-PSDB; AAA30727.
XX PT Non-endogenous constitutively activated human G protein-coupled
XX PT receptors, useful for identifying agonists for use as pharmaceutical
XX PT agents.
XX PS Example 2; Page 254-256; 341pp; English.

XX The invention relates to constitutively active, non-endogenous versions
XX of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
XX CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
XX CC and AAA30775-A30779). The mutant proteins of the invention contain a
XX CC mutation in a portion of the protein comprising intracellular loop 3
XX CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
XX CC is substituted for an endogenous residue in IC3 at a position 16 amino
XX CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
XX CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
XX CC Ala, and is preferably Lys. When the endogenous residue at this position
XX CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
XX CC amino acid stretch between the substituted amino acid and the Pro may be

CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. Sequences AAY90643-
CC AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
XX SQ Sequence 372 AA;

Query Match 99.7%; Score 1947; DB 3; Length 372;

Best Local Similarity 99.7%; Pred. No. 7.5e-196;

Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNYPTLEMDLENLEDFWELDRLDYNDTSLVENHLCPTATGFLMASPKAVFPVAYSL 60
Db 1 MNYPTLEMDLENLEDFWELDRLDYNDTSLVENHLCPTATGFLMASPKAVFPVAYSL 60
Qy 61 IFLLGVIGNVLVLVILSRHQTRSTETFLFHLAVADLLLVILPFAVAGSVGVVLGTF 120
Db 61 IFLLGVIGNVLVLVILSRHQTRSTETFLFHLAVADLLLVILPFAVAGSVGVVLGTF 120
Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHYRHRLLSIHITCGTIWLVGFL 180
Db 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHYRHRLLSIHITCGTIWLVGFL 180
Qy 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
Db 181 ALPEILPAKVSQGHNNLSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
Qy 241 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
Db 301 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 15

ADC22719
ID ADC22719 standard; protein; 372 AA.
XX AC ADC22719;
XX DT 18-DEC-2003 (first entry)
XX DE Human G protein-coupled receptor (GPCR) polypeptide #58.
XX KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
XX KW intracellular-3 region; IC3; receptor.
XX OS Homo sapiens.
XX PN US6555339-B1.
XX PD 29-APR-2003.
XX PF 13-OCT-1998; 98US-00170496.
XX PR 14-APR-1997; 97US-00839449.
XX PR 14-APR-1998; 98US-00060188.
XX PR 26-JUN-1998; 98US-0090783P.
XX PR 07-AUG-1998; 98US-0095677P.
XX PA (AREN-) ARENA PHARM INC.

XX Liaw CW, Behan DP, Chalmers DT;
XX WPI; 2003-742861/70.
DR N-PSDB; ADC22718.
XX
PT Creating a constitutively active version of an endogenous human G protein
PT coupled receptor (GPCR) comprises substituting a specific amino acid in
PT the transmembrane-6 region with a different amino acid, and testing for
PT constitutive activity.
XX
XX Example 2; SEQ ID NO 200; 221pp; English.
PS
XX
CC The invention relates to a method for treating a non-endogenous,
CC constitutively active version of an endogenous human G protein-coupled
CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an
CC intracellular-3 (IC3) region, by substituting a specific amino acid in
CC the TM6 region with a different amino acid, and testing for constitutive
CC activity. The method is useful for creating a constitutively active
CC version of an endogenous human GPCR that comprises a transmembrane 6
CC region and an intracellular loop 3 region. The altered human GPCR
CC polypeptides are useful for screening test compounds for identification
CC of inverse agonists or partial agonists of GPCR polypeptides, which may
CC have therapeutic uses. The altered GPCRs may also be used in vivo or in
CC vitro in biological research. A nucleic acid encoding the altered GPCR
CC may be used to create a transgenic animal expressing the altered GPCR.
CC The method allows screening for compounds that modulate the activity of a
CC human G protein-coupled receptor without the need for provision of a
CC ligand for the receptor. This is particularly useful in allowing
CC screening of compounds against orphan receptors for which no ligand is
CC currently known. This sequence represents a human GPCR polypeptide of the
XX invention.
XX
SQ Sequence 372 AA;
.
Query Match 99.7%; Score 1947; DB 7; Length 372;
Best Local Similarity 99.7%; Pred. No. 7.5e-196;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNYPLTELDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTELDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
QY 61 IFLLGVIGNVLVLILERHQRSTSTETFLFLAVADLLVFLPFAVAEGSVGWVLTGF 120
DB 61 IFLLGVIGNVLVLILERHQRSTSTETFLFLAVADLLVFLPFAVAEGSVGWVLTGF 120
QY 121 LCKTVIALHKVNYFCSSLLACIADRYLAIVHAVHAYRHRRLLSHITCGTILWVGFL 180
DB 121 LCKTVIALHKVNYFCSSLLACIADRYLAIVHAVHAYRHRRLLSHITCGTILWVGFL 180
QY 181 ALPEILLFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILLFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPRQAKRVAILVTSIFFLCWSPYHIVIFLDTLAKLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQAKRVAILVTSIFFLCWSPYHIVIFLDTLAKLKAVDNTCKLNGSL 300
QY 301 PVAITWCEFLGLAHCCNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
DB 301 PVAITWCEFLGLAHCCNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: August 29, 2005, 23:47:36 ; Search time 41 Seconds
(without alignments)
872.991 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPLTLEMDLENLEDFWE.....PSWRRSSLSSENATSLTTF 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	372	2 S26667	G protein-coupled
2	1700	87.0	327	2 S56162	MDCR15 protein - h
3	1635	83.7	374	2 S42628	G protein-coupled
4	1590	81.4	374	2 S32785	G protein-coupled
5	615	31.5	367	2 JE0349	interferon-inducib
6	601.5	30.8	360	2 A53611	interleukin-8 rece
7	596	30.5	378	2 B55735	lymphocyte-specifi
8	574	29.4	378	2 A45680	G protein-coupled
9	571.5	29.3	378	2 A55735	G protein-coupled
10	569	29.1	355	2 JQ1231	interleukin-8 rece
11	561	28.7	350	2 A39445	interleukin-8 rece
12	547	28.0	358	2 A53752	interleukin-8 rece
13	543	27.8	352	2 G00048	fusin (FUSRA) - c
14	540	27.6	352	2 A45747	neuropeptide Y/pep
15	537.5	27.5	353	2 S28787	neuropeptide Y/pep
16	536	27.4	356	2 S42096	interleukin-8 rece
17	519.5	26.6	359	2 A48921	interleukin-8 rece
18	499.5	25.6	354	2 A23669	interleukin-8 rece
19	497	25.4	355	2 JCS067	G protein-coupled
20	495.5	25.4	360	2 JC4587	chemokine (C-C) re
21	494.5	25.3	369	2 JCS068	G protein-coupled
22	479.5	24.6	360	2 A51160	chemokine (C-C) re
23	474	24.3	355	2 I49339	macrophage inflam
24	465	23.8	360	2 JC2443	chemokine (C-C) re
25	461.5	23.6	354	2 I58186	probable G protein
26	461.5	23.6	374	2 I38450	chemokine (C-C) re
27	461	23.6	352	2 A43113	chemokine (C-C) re
28	455	23.3	355	2 A55177	chemokine (C-C) re
29	450	23.0	383	2 S55594	G protein-coupled

30	449.5	23.0	355	2 JC4304	orphan G protein-c
31	449	23.0	355	2 G02436	chemokine (C-C) re
32	442.5	22.7	350	2 JN0621	G protein-coupled
33	441	22.6	354	2 B55733	G protein-coupled
34	437	22.4	359	2 I49341	MIP-1 alpha recept
35	432	22.1	333	2 I65989	G protein-coupled
36	429	22.0	362	2 JN0694	angiotensin II rec
37	415	21.2	359	2 S15403	angiotensin II rec
38	408	20.9	359	2 JC2134	angiotensin II rec
39	406	20.8	359	2 JC1104	angiotensin II rec
40	406	20.8	359	2 JH0621	angiotensin II rec
41	406	20.8	371	2 JCS498	G protein-coupled
42	404.5	20.7	362	2 A30341	G protein-coupled
43	403.5	20.7	356	2 I49340	MIP-1 alpha recept
44	402	20.6	359	2 A48857	angiotensin II rec
45	402	20.6	371	2 JCS796	probable chemoattr

ALIGNMENTS

RESULT 1

S26667
G protein-coupled receptor BLR1 - human
C.Species: Homo sapiens (man)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: S26667
R.Dobner, T.; Wolf, I.; Emrich, T.; Lipp, M.
Eur. J. Immunol. 22, 2795-2799, 1992
A.Title: Differentiation-specific expression of a novel G protein-coupled receptor fro
A.Reference number: S26667; MUID:93049615; PMID:1425907
A.Accession: S26667
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-372 <DOB>
A.Cross-references: UNIPROT:P32302; EMBL:X68149; NID:G29459; PIDN:CAA48252.1; PID:G294
C.Genetics:
A.Gene: GDB:BLR1
A.Cross-references: GDB:I36235; OMIM:601613
A.Map position: 15q26.1-15q26.1
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; transmembrane protein

Query Match	100.0%	Score	1953;	DB	2;	Length	372;
Best Local Similarity	100.0%	Pred. No.	1.7e-162;				
Matches	372;	Conservative	0;	Mismatches	0;	Indels	0;
Gap	0;						
Qy	1	MNYPLTLEMDLENLEDFWELDRDNYNDTSLVENHLCPTGELMASFKAVFPVAYSL	60				
Db	1	MNYPLTLEMDLENLEDFWELDRDNYNDTSLVENHLCPTGELMASFKAVFPVAYSL	60				
Qy	61	IFLLGVIGNVLVILERHROTSTETFLFHLAVADLLVFLPFAVAGSVGWVLTGF	120				
Db	61	IFLLGVIGNVLVILERHROTSTETFLFHLAVADLLVFLPFAVAGSVGWVLTGF	120				
Qy	121	LCKTVIALHKVNFYCSSLLACIAVDRLAIVHVAHYHRRLLSIHITCGITWLVGFL	180				
Db	121	LCKTVIALHKVNFYCSSLLACIAVDRLAIVHVAHYHRRLLSIHITCGITWLVGFL	180				
Qy	181	ALPELTFKAVSQGHNNISPRCTESQENQAETHAFTSRFLYHVAGFLPMLVMGWCYVG	240				
Db	181	ALPELTFKAVSQGHNNISPRCTESQENQAETHAFTSRFLYHVAGFLPMLVMGWCYVG	240				
Qy	241	VVHLRQQRQPQRKAVRVAILVTSIFFLCWSPHYHIFLDTLARLKAVDNCKLNGSL	300				
Db	241	VVHLRQQRQPQRKAVRVAILVTSIFFLCWSPHYHIFLDTLARLKAVDNCKLNGSL	300				
Qy	301	PVAITMCBFLGLAHCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLPFSWRRSSL	360				
Db	301	PVAITMCBFLGLAHCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLPFSWRRSSL	360				
Qy	361	SESENATSLTTF	372				

C;Keywords: G protein-coupled receptor; transmembrane protein

	Query Match Best Local Similarity Matches	29.4%; 35.9%; 126;	Score 574; Pred. No. 2.2e-42; Conservative 78;	DB 2; Mismatches 125; Indels 22;	Gaps 9;
QY	29	DTSLVENHLCPATEGPLMASPKAVFPVPVAYSLSIFLLGVIGNVGLVLILVRHRQTSSSTET	88		
Db	40	DYTLFES-LCSKKD---VRNFKAWFPLIMYSIIICFGLLGNLGLVVLTYYFKRLKMTMDT	95		
QY	89	FULFLHAVADLLLVFLTPFAVAEGSVGWLGTFLCKTVIALHKWNPFCYSLLIACIADVRY	148		
Db	96	YLNLNAVADIPELLFTLPFWAASAKSWFGVFCKLIPAIYMSPFSKWLLLLCISIDRY	155		
QY	149	LAIHVAHAYRHR--LLSIHIHTCTGIWLVGFLALPEILPAKVSGQHNNSLPRCTFSQ	206		
Db	156	VAILQAVSARHRRARVLLISKLCVGSAILATVLSIPLELLSYDLQRSSEQAM-RCSLIT	214		
QY	207	ENOETHAWFTSRFYHYHAGVELLPMLVNGWCYGVVHHLRQAQRPPQOKAVRVAILUTS	266		
Db	215	EH---VEAFITIQVAQMVIQGLFVLPLLMAFSFCYLVIRTLQA-RNFERNKAIKIIVVV	270		
QY	267	IFFELCWSPYHIVI FLDTLRLKAVNDNTCKINGSLPVAITMCFEFLCLAHCCLNBMLYTPAG	326		
Db	271	VFIVEQLPGVVLTAQTVANFNITSCELSKQLNIADVTYSIACVRCVWNPIFYAPIG	330		

	QY	327 VFRSRLTLTKLGCTGASLQLPSFW-----RRSLSESENATSLT 370
		:
		::
	D6	331 VFVRNDFIKFLKDLGLCLSGEQLRQ----WSSCRHRRSSMSVEATTTTTTS 377
		:
		:

RESULT 9
A55735

C;Specimen: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A55735

Genomics 23, 643-650, 1994
A, Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A, Reference number: A55735; PMID:95154835; PMID:7851893
A, Accession number: U00000

A;Accession: A35735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>

A;Cross-references: UNIRAOI:P4774; GS:DJL360; NIB:G960340; EMBL:U00001.1; EMBL:U00002.1; EMBL:U00003.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 29.3%; Score 3/1.5; DB 2; Length 3/6;
Best Local Similarity 36.7%; Pred. No. 3.6e-42;
Matches 120; Conservative 71; Mismatches 129; Indels 7; Gaps 4;

QY	48	SFAKVFVAYSLIFLLGVGNVLVLLERHKHQIKSSIEFLLHVAUULLVLFPA	107
Db	55	NFKAWFLPLMYSVICFVGLLGNGLVILTYIYFKRLKLTMTDTYLLNLAVADILFLLIIPFW	114

[illegible]

Qy	166	IHTCTG	WLVGF	LALP	IFAKV	SGOH	HNNS	LPCT	FSQEN	QAE	THA	WTF	SR	FL	XHVA	225	
		:	:	:	:	:	:	:	:	:	:	:	:	:	:		
		:	:	:	:	:	:	:	:	:	:	:	:	:	:		
		:	:	:	:	:	:	:	:	:	:	:	:	:	:		
db	175	SKLSCV	GIWML	ALFSL	IPELLY	SGLQ	KN	SGED	TL	RC	SLV	--	SAQ	VEAL	ITIQ	VAOMVF	230

[illegible]

QY : : : : :
286 RLKAVDNTCKLNGSLPVALTMCBFLGHAHCCLNPMLYTFAGVKPRSDLSRLLLKLGCTGP 345
Db : : : : :
290 NFNIITNSCETSQQLNIAYDVVTSLSVRCCVNPFYAFGVGKFRSDDLKLFNDLGCSIQ 349

QY 346 ASLCQLPFWRRSSLSSENATSTTTF 372
DB 350 ERLRHWSRCRHVRNASVSMEEATTTTF 376

RESULT 10

QJ1231
interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, J.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: QJ1231; MUID:91378994; PMID:1898400
A:Accession: QJ1231
A:Molecule type: DNA
A:Residues: 1-355 <BEC>
A:Cross-references: UNIPROT:P21109; GB:M74240; NID:G165439; PIDN:AAA31375.1; PID:G165439
R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A:Reference number: A46483; MUID:92148149; PMID:1737938
A:Accession: A46483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEE>
A:Cross-references: GB:M82873; NID:G165440; PIDN:AAA31376.1; PID:G165441
A:Experimental source: neutrophils
A>Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:P:81530)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.1%; Score 569; DB 2; Length 355;
Best Local Similarity 38.3%; Pred. No. 5.6e-42;
Matches 129; Conservative 52; Mismatches 146; Indels 10; Gaps 7;

QY 7 LEMDLNLEDLF-WELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSLIFLLG 65
DB 1 MEYVNMNTDLMTWFEDEFANATGMPPEKDYSPCL--VTQTINKVYVVVYIAYLVFLS 58
QY 66 VIGNVLVLVLEHRQTRSTETFLHLAVADLLLVFILPFAVAGSVGVLGTFLCKTV 125
DB 59 LLGNSLVMLVILYSRNSRSTVDVYLLNLMADLLFALTMTPEIWAHSVKEGWFGTPLCKV 118
QY 126 IALHKVNFYCSLLACIADRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFLALPEI 195
DB 119 SLVKEVNFYSGILLACISVDRLAIVHATRTLTQKRHL-VKFCVLCGWSLILSLPFF 177
QY 186 LFAKVSQGHNNSLPRTCTFSQENQAETHAW-FTSRFLYHVAGFLPMLVMGVCYGVVHR 244
DB 178 LFRQVFS--PNNSPVC--YEDLGHTAKRMVLRILPHTFGFILPLVLMFCYGTFLT 233
QY 245 LRAQRRPQOKAVRVAILVTSIFFLCWSPYHIVFDLTARLKAVENTCKLNGSLPVAI 304
DB 234 LFQA-HMGQKRAMRVIFAVVLLCWLPLYNLVLLADTLMTHTVQETCQRNDIDRAL 292
QY 305 TWCEFLGLAHCLNPMLYTPAGVKFRSDLSRLTLKLG 341
DB 293 DATEILGFLHSLNPIIYAFIGNFRNGFLKMLAARG 329

RESULT 11

A39445
interleukin-8 receptor type A - human
N:Alternate names: interleukin-8 receptor, high-affinity
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: I37449; I38711; I38711; A39445
R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region
A:Reference number: I37449; MUID:93252387; PMID:8486366

A:Accession: I37449
A:Molecule type: DNA
A:Residues: 1-350 <RES>
A:Cross-references: UNIPROT:P25024; EMBL:X65858; NID:G312046; PIDN:CAA46688.1; PID:G312046
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8.
A:Reference number: I37898; MUID:95014476; PMID:7929358
A:Accession: I38710
A:Molecule type: DNA
A:Residues: 1-350 <RE2>
A:Cross-references: EMBL:U11870; NID:G511804; PIDN:AAA64378.1; PID:G511805
A:Accession: I38711
A:Molecule type: mRNA
A:Residues: 1-16 <RE3>
A:Cross-references: EMBL:U11871; NID:G511806; PIDN:AAA64379.1; PID:G733002
R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A:Title: Structure and functional expression of a human interleukin-8 receptor.
A:Reference number: A39445; MUID:91368199; PMID:1840701
A:Accession: A39445
A:Molecule type: mRNA
A:Residues: 1-275, 'T', 277-350 <HOL>
A:Cross-references: GB:M68932; NID:G186369; PIDN:AAA59159.1; PID:G186370
C:Genetics:
A:Gene: GDB:IL8RA
A:Cross-references: GDB:135039; OMIM:146929
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 28.7%; Score 561; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 2.8e-41;
Matches 137; Conservative 55; Mismatches 149; Indels 22; Gaps 11;

QY 11 LENLED-LFWELDRLDNYNDTSLVENHLCPCATE--GPLMASFKAV---FVPVAYSLIFLL 64
DB 1 MSNITDPPQWDFDDL---NFTGMP-----PADEDYSPCMLETLNKKYVYIIAYALVFL 52
QY 65 GVIGNVLVLVLEHRQTRSTETFLHLAVADLLLVFILPFAVAGSVGVLGTFLCKT 124
DB 53 SLIGNSLVMLVILYSRVGRSTVDVYLLNLMADLLFALTMTPEIWAHSVKEGWFGTFLCKV 112
QY 125 VIALHKVNFYCSLLACIADRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFLALPE 184
DB 113 VSLLEKVNPFYSGILLACISVDRLAIVHATRTLTQKRHL-VKFCVLCGWSLNMISLPF 171
QY 185 ILFAKVSQGHNNSLPRTCTFSQENQAETHAW-FTSRFLYHVAGFLPMLVMGVCYGVVH 243
DB 172 LFRQAY--HPNNSPVCYEVILGN--DTAKRMVLRILPHTFGFILPFLVLMFCYGTFL 227
QY 244 LRAQRRPQOKAVRVAILVTSIFFLCWSPYHIVFDLTARLKAVENTCKLNGSLPVA 303
DB 228 LTFKA-HMGQKRAMRVIFAVVLLCWLPLYNLVLLADTLMTHTVQIQCSCERRNIGRA 286
QY 304 ITWCEFLGLAHCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCO-LFPSRRSLSE 362
DB 287 LDATILGFLHSLNPIIYAFIGNFRNGFLKMLAHLVSKFELARHVRVTSYTSSSVNV 346
QY 363 SEN 365
DB 347 SSN 349

RESULT 12

A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Naval J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A;Reference number: A53752; MUID:94230294; PMID:8175642

A;Accession: A53752

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-358 <PRA>

A;Cross-references: UNIPROT:P35344; GB:L24445; NID:G437661; PIDN:AAA13378.1; PID:G437662

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.0%; Score 547; DB 2; Length 358;
Best Local Similarity 37.2%; Pred. No. 4.7e-40;
Matches 137; Conservative 50; Mismatches 163; Indels 18; Gaps 9;

Qy 8 EMDLEN--LEDLFWELDRLDNYND--TSLVENHLCPATGELPMLFASFAVFPVAYSILFL 63

Db 3 EFTWENYSYEDFFGDFSNYSYSTDLPTLLDSAPCRSES---LETNSYVVLITYILVFL 58

Qy 64 LGVIGNVLVLILHRHQTRSSSTTFPLHLAVADLLVFLPFAVAGSGVWGLPFLCK 123

Db 59 LSLGNSLMLVILYSRSTCVTDVYLLNLAIDLLFATLPIWAASKVHGWTGTPFLCK 118

Qy 124 TVIALHKVNFVCSLLACIADRYLAIHVAVHAYRHRLLSIHITCGTTLWGLFLLALP 183

Db 119 VSLVKEVNFVSGILLACISVDRIYLAIVHATRTMIQRHL-VKFICLSMWGSLLISLP 177

Qy 184 EILPAKVSQGHNNLSLPRCTFSSQENQAETHAW-FTSRFLYHVAGFLPLMLVMGVCYGVV 242

Db 178 ILILFRNAI--PPPNSSPVCVEDMGN--STAKRMVLAILQTGFIPLVLMFLFCVFTL 233

Qy 243 HRLRQARRRQKQAVRAILVTSIFFLCWSPHYIVFLDTLARKLAVDNTCKLNSLPV 302

Db 234 RTLFQA-HMGQKRAMRVIFAVLLIFLLCWLPLYNLVLLTDLRTHVIOETCERRNDIDR 292

Qy 303 AITWCEFLGHAHCLNPMLYTFAGVKFRSDLSRLTLKGTGTPASLCQLFPSSRRSLSE 362

Db 293 ALDQATEILGFLHSCNFIYAFIGQKPRYGLLKILAAHGLISKEFLAK---ESRPFVAS 349

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

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Qy 363 SENATSLT 370

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Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 219 RELYHVAGFLPLMLVMGVCYGVVHRLRQARRPQKAVRAVILVTSIFFLCWSPHYV 278

Db 200 QFQHMVGLILPGVILSCVCIISKLSHSGH-QKRKALKTTVILILAFACWLPYIG 258

Qy 279 IFDLTLARLKAVDNTCKLNSLPVATMCEFLGHAHCLNPMLYTFAGVKFRSDLSRLIT 338

Db 259 ISIDSFILLEIHKQCEFTVHKWISITTEALGFHCHCLNPLIYALFGAKFKTSAQHALT 318

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

Qy 339 KLGTGTPASLCQLFPSSRRSSLS-ESENAAT 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSSS 348

RESULT 14

A45747

N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LBSTR;

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence revision 03-May-1994 #text change 09-Jul-2004

C;Accession: A45747; A53103; I53006; I59444; I69203; S32761

R;Fedeerspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lu

Genomics 16, 707-712, 1993

A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a

A;Reference number: A45747; MUID:93315164; PMID:8325644

A;Accession: A45747

A;Molecule type: mRNA

A;Residues: 1-352 <PDR>

A;Cross-references: UNIPROT:P61073; GB:M99293; NID:G292516; PIDN:AAA16617.1; PID:G292;

R;Joetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A;Title: Cloning of a human seven-transmembrane domain receptor, LBSTR, that is highl;

A;Reference number: A53103; MUID:94103215; PMID:8276799

A;Accession: A53103

A;Molecule type: mRNA

A;Residues: 1-352 <LOE>

A;Cross-references: EMBL:X71635; NID:G297099; PIDN:CAA50641.1; PID:G297100

R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A;Title: Molecular cloning, characterization, and localization of the human homolog t

A;Reference number: I53006; MUID:93319629; PMID:8329116

A;Accession: I53006

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-352 <HER>

A;Cross-references: GB:L06797; NID:G414929; PIDN:AAA03209.1; PID:G414928

R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; I

Regul. Pept. 47, 247-258, 1993

A;Title: A proposed bovine neurotrophin Y (NPY) receptor cDNA clone, or its human hom

A;Reference number: I59444; MUID:94052833; PMID:8234909

A;Accession: I59444

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-352 <RE2>

A;Cross-references: GB:L01639; NID:G189313; PIDN:AAA16594.1; PID:G189314

R;Nimura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c

A;Reference number: I54751; MUID:94092629; PMID:7505609

A;Accession: I63203

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-352 <RES>

A;Cross-references: GB:D10924; NID:G219868; PIDN:BA01722.1; PID:G219869

C;Genetics: GDB:NPY3R; NPY3

A;Cross-references: GDB:230002; OMIM:162643

A;Map position: 2q21-2q21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 540; DB 2; Length 352;

Best Local Similarity 33.9%; Pred. No. 1.9e-39;

Qy 47 ASKAVPVPVAYSILFLGIVGNVLVLILVILHRQTRSSSTETFLHLAVADLLVFLTPP 106

Db 34 AHNRIPLPTIYSIFITGVINGNLVGMVYQKRSMTDKYRLHLVSADLLVYVTLPP 93

Qy 107 AVAGSGVWGLTGLCKTVIALHKVNFVCSLLACIADRYLAIHVAVHAYRHRLLSI 166

Db 94 WADAVANVWFNGFLCKAVHVIYTVNLYSSVLIILAFISLDRLAIHVHATNSQRPKLAE 153

Qy 167 HITCGTTLWVGLFLLALPEILFAKVSQG-----HNNSLPRCTTSQENQAETHAW

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:46:51 ; Search time 173 Seconds
(without alignments)
1101.118 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPLFLEMDLEDFWE.....PSWRSSSESNATSLTTF 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.:

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1953	100.0	372	1 CCR5 HUMAN	P32302 homo sapien
2	1638	83.9	374	2 Q6P3C2	Q6P3C2 mus musculus
3	1635	83.7	374	1 CCR5 MOUSE	Q04683 mus musculus
4	1590	81.4	374	1 CCR5 RAT	P34997 rattus norv
5	866.5	44.4	392	2 Q93281	Q93281 gallus gall
6	646	33.1	366	2 Q867B2	Q867B2 capra hircu
7	638.5	32.7	390	2 Q6GNE2	Q6GNE2 xenopus lae
8	635	32.5	368	1 CCR3 HUMAN	P49682 homo sapien
9	635	32.5	415	2 Q72710	Q72710 homo sapien
10	615	31.5	367	2 Q9QW6	Q9QW6 mus musculus
11	614	31.4	367	1 CCR3 MOUSE	Q8410 mus musculus
12	613	31.4	367	2 Q9J119	Q9J119 rattus norv
13	607	31.1	374	2 Q802H1	Q802H1 petromyzon
14	606	31.0	355	2 Q8HZN4	Q8HZN4 cercopithe
15	601.5	30.8	355	2 Q8HZN8	Q8HZN8 pan troglod
16	601.5	30.8	360	1 IL8B HUMAN	P25025 homo sapien
17	599.5	30.7	355	2 Q8HZN5	Q8HZN5 macaca mula
18	596.5	30.5	355	2 Q8HZN7	Q8HZN7 gorilla gor
19	596	30.5	378	1 CKR7 HUMAN	P32248 homo sapien
20	595	30.5	378	2 Q8H2R6	Q8H2R6 macaca mula
21	594.5	30.4	353	1 IL8B PANTR	Q28807 pan troglod
22	590.5	30.2	355	2 Q8H2N3	Q8H2N3 papio hamad
23	585.5	30.0	353	1 IL8B GORGO	Q28422 gorilla gor
24	579.5	29.7	353	1 IL8B MACMU	Q28519 macaca mula
25	577.5	29.6	352	2 Q810T4	Q810T4 cavia porce
26	576.5	29.5	378	2 Q8CAS2	Q8CAS2 mus musculus
27	576	29.5	380	2 Q861S1	Q861S1 sus scrofa
28	575	29.4	378	2 Q6U2D6	Q6U2D6 rattus norv
29	571.5	29.3	378	1 CKR7 MOUSE	P47774 mus musculus
30	569	29.1	355	1 IL8A RABIT	P21109 oryctolagus
31	568.5	29.1	355	2 Q8H2N6	Q8H2N6 pongo pygma

RESULT 1

CCR5_HUMAN

ID_CCR5_HUMAN STANDARD; PRT; 372 AA.

AC P32302; Q14811;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma

DE receptor 1) (Monocyte-derived receptor 15) (MDR15).

GN Name=BLR1; Synonyms=CXCR5;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A. (ISOFORM LONG).

RC TISSUE=Lymphocytes; PubMed=1425907;

RX MEDLINE=93049615; PubMed=1425907;

RA Dobner T., Wolf I., Emrich T., Lipp M.;

RT "Differentiation-specific expression of a novel G protein-coupled

RT receptor from Burkitt's lymphoma.";

RL Eur. J. Immunol. 22:2795-2799(1992).

RN [2]

SEQUENCE FROM N.A. (ISOFORM SHORT).

RC TISSUE=Blood;

RX MEDLINE=95366951; PubMed=7639692;

RA Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;

RT "Sequence variation of a novel heptahelical leucocyte receptor through

RT alternative transcript formation.";

RL Biochem. J. 309:773-779(1995).

RN [3]

LIGAND BINDING.

MEDLINE=98130629; PubMed=9463416;

RA Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,

RA Baggiolini M., Moser B.;

RT "B cell-attracting chemokine 1, a human CXC chemokine expressed in

RT lymphoid tissues, selectively attracts B lymphocytes via BLR1/CXCR5.";

RL J. Exp. Med. 187:655-660(1998).

CC -!- FUNCTION: Cytokine receptor that binds to BLC. BLR1 exerts

CC possibly a regulatory function in burkitt lymphoma (BL)

CC lymphomagenesis and/or B-cell differentiation. It is a potential

CC candidate for cell-cell interaction, and activation of mature B-

CC lymphocytes in lymphatic tissues.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=P32302-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=P32302-2; Sequence=VSP_001892;

CC -!- TISSUE SPECIFICITY: Expression in mature B-cells and Burkitt

CC lymphoma cells.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

QY 1 MNYPLTLEMD--LENLEDFWELDRDLNNDYNTSLVENHLCPCATGEGPLMASFKAVFPVAY 58
 Db 1 MNYPLTLDGMSITYNDDLYKELAFYSNSTEIPLOQDSNFCSTVEGELLTSFKAVFPVAY 60
 QY 59 SLIFLLGVGNVLVILERHRTSRSTETFLFHLAVADLLVFLPFAVAEGSVGWVLG 118
 Db 61 SLIFLLGMGNILVILERHRTSRSTETFLFHLAVADLLVFLPFAVAEGSVGWVLG 120
 QY 119 TFLCKTVIALHKVNFYCSSLLACIAVDRLAIVHAVYHRRLLSIHITCTIWLGVF 178
 Db 121 TFLCKTVIALHKVNFYCSSLLACIAVDRLAIVHAVYHRRLLSIHITCTIWLGVF 180
 QY 179 LLALPEILPAKVSCQGHNNSLPCTFSQENOAETHAWFTSRFLYHVGELLPLMVGWY 238
 Db 181 LFLALPELLFAKVQGHNNDSLPQCTFSQENAEATRAWFTSRFLYHGGELLPLMVGWY 240
 QY 239 VGVVHRLQORRQKQKAVRVAILVTSIFFLCWSPHIVIFLDTLRLKAVDNTCKLNG 298
 Db 241 VGVVHRLQORRQKQKAVRVAILVTSIFFLCWSPHIVIFLDTLRLKAVDNTCKLNG 300
 QY 299 SLPVAITMCEFLGLAHCLLPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPWSRRS 358
 Db 301 YLSVAITLCEFLGLAHCLLPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPWSRRS 360
 QY 359 SLSESENATSLTTF 372
 Db 361 SLSESENATSLTTF 374
 RESULT 3
 CCR5_MOUSE STANDARD; PRT; 374 AA.
 AC Q04683;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma receptor 1 homolog).
 GN Name=BLR1; Synonyms=Cxcr5, Gpcr6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94009211; PubMed=8405054;
 RA Kaiser E., Foerster R., Wolf I., Epensperger C., Kuehl W.M., Lipp M.;
 RT "The G protein-coupled receptor BLR1 is involved in murine B cell differentiation and is also expressed in neuronal tissues.";
 RL Eur. J. Immunol. 23:2532-2539(1993).
 RN [2]
 RP SEQUENCE OF 151-269 FROM N.A.
 RC TISSUE=testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RT "Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=97133211; PubMed=8978608; DOI=10.1016/S0092-8674(00)81798-5;
 RA Foerster R., Mattis A.E., Kremmer E., Wolf E., Brem G., Lipp M.;
 RT "A putative chemokine receptor, BLR1, directs B cell migration to defined lymphoid organs and specific anatomic compartments of the spleen.";
 RL Cell 87:1037-1047(1996).
 RN [4]
 RP LIGAND BINDING.
 RX MEDLINE=98146056; PubMed=9486651; DOI=10.1038/35876;
 RA Gunn M.D., Ngo V.N., Ansel K.M., Ekland E.H., Cyster J.G., Williams L.T.;

RT "A B-cell-homing chemokine made in lymphoid follicles activates Burkitt's lymphoma receptor-1.";
 RL Nature 391:799-803(1998).
 CC -!- FUNCTION: Cytokine receptor that binds to B lymphocyte chemoattractant (BLC). Involved in B-cell migration into B-cell follicles of spleen and Peyer's patches, but not in those of mesenteric or peripheral lymph nodes.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly in spleen, in resting B-cells.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC -----
 CC EMBL, X71788; CAA50673.1; -;
 DR EMBL, L20332; AAA16852.1; -;
 DR PIR, S42628; S42628.
 DR MGI, MGI:103567; BLR1.
 DR InterPro: IPR000248; Angtn2 receptor.
 DR InterPro: IPR001053; CXCR5 Receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam, PF00001; 7tm_1; 1.
 DR PRINTS, PR00241; ANGIOTENSINR.
 DR PRINTS, PR00564; CXCR5_KINERS.
 DR PRINTS, PR00237; GPCR_HODOPSIN.
 DR PROSITE, PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE, PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR B-cell activation; G-protein coupled receptor; Glycoprotein; Transmembrane.
 KW DOMAIN 1 57 Extracellular (Potential).
 FT TRANSMEM 58 78 1 (Potential).
 FT DOMAIN 79 90 Cytoplasmic (Potential).
 FT TRANSMEM 91 111 2 (Potential).
 FT DOMAIN 112 126 Extracellular (Potential).
 FT TRANSMEM 127 147 3 (Potential).
 FT DOMAIN 148 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 190 4 (Potential).
 FT DOMAIN 191 221 Extracellular (Potential).
 FT TRANSMEM 222 242 5 (Potential).
 FT DOMAIN 243 261 Cytoplasmic (Potential).
 FT TRANSMEM 262 282 6 (Potential).
 FT DOMAIN 283 306 Extracellular (Potential).
 FT TRANSMEM 307 327 7 (Potential).
 FT DOMAIN 328 374 Cytoplasmic (Potential).
 FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
 FT DISULFID 124 204 Potential.
 SQ SEQUENCE 374 AA; 42100 MW; 385258420C1EDE30 CRC64;
 Query Match 83.7%; Score 1635; DB 1; Length 374;
 Best Local Similarity 82.9%; Pred.No. 7.1e-104;
 Matches 310; Conservative 29; Mismatches 33; Indels 2; Gaps 1;
 QY 1 MNYPLTLEMD--LENLEDFWELDRDLNNDYNTSLVENHLCPCATGEGPLMASFKAVFPVAY 58
 Db 1 MNYPLTLDGMSITYNDDLYKELAFYSNSTEIPLOQDSNFCSTVEGELLTSFKAVFPVAY 60
 QY 59 SLIFLLGVGNVLVILERHRTSRSTETFLFHLAVADLLVFLPFAVAEGSVGWVLG 118
 Db 61 SLIFLLGMGNILVILERHRTSRSTETFLFHLAVADLLVFLPFAVAEGSVGWVLG 120
 QY 119 TFLCKTVIALHKVNFYCSSLLACIAVDRLAIVHAVYHRRLLSIHITCTIWLGVF 178
 Db 121 TFLCKTVIALHKVNFYCSSLLACIAVDRLAIVHAVYHRRLLSIHITCTIWLGVF 180
 QY 179 LLALPEILPAKVSCQGHNNSLPCTFSQENOAETHAWFTSRFLYHVGELLPLMVGWY 238
 Db 181 LFLALPELLFAKVQGHNNDSLPQCTFSQENAEATRAWFTSRFLYHGGELLPLMVGWY 240

QY 239 VGVHRLRQARRPQKQKAVRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVENTCKING 238
 DB 241 VGVHRLRQARRPQKQKAVRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVENTCKING 300
 QY 299 SLPAITMCEFLGHAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRS 358
 DB 301 YLSVAITLCEFLGHAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRS 360
 QY 359 SLSESENATSLTTF 372
 DB 361 SLSESENATSLTTF 374

RESULT 4
 CCR5_RAT
 ID_CCR5_RAT STANDARD; PRT; 374 AA.
 AC P34997;
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma receptor 1 homolog) (Neurolymphatic receptor) (NLR).
 DE receptor 1 homolog (Neurolymphatic receptor) (NLR).
 GN Name=Blri; Synonyms=Cxcr5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=93238948; PubMed=8386678; DOI=10.1016/0014-5793(93)80102-Z;
 RA Kouba M., Vanetti M., Wang X., Schaefer M., Hoellit V.;
 RT Cloning of a novel putative G-protein-coupled receptor (NLR) which is expressed in neuronal and lymphatic tissue.;
 RL FEBS Lett. 321:173-178(1993).
 CC -1- FUNCTION: Cytokine receptor that binds to B lymphocyte chemottractant (BLC) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in neuronal and lymphatic tissue.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC
 CC EMBL: X71463; CAA50582.1; -
 CC PIR: S32785; S32785.
 CC RGD: 62010; Blri.
 CC InterPro: IPR000248; Angntn2_receptor.
 CC InterPro: IPR001053; CXCR5_receptor.
 CC InterPro: IPR000276; GPCR_Rhodopsin.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00241; ANGIOTENSINR.
 CC PRINTS: PR00564; CXCR5_KINERS.
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
 CC B-cell activation, G-protein coupled receptor; Glycoprotein; Transmembrane.
 KW Transmembrane. 1 57 Extracellular (Potential).
 FT DOMAIN 58 78 1 (Potential).
 FT TRANSMEM 58 78 1 (Potential).
 FT DOMAIN 79 90 Cytoplasmic (Potential).
 FT TRANSMEM 91 111 2 (Potential).
 FT DOMAIN 112 126 Extracellular (Potential).
 FT TRANSMEM 127 147 3 (Potential).
 FT DOMAIN 148 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 190 4 (Potential).
 FT DOMAIN 191 221 Extracellular (Potential).

FT TRANSMEM 222 242 5 (Potential).
 FT DOMAIN 243 261 Cytoplasmic (Potential).
 FT TRANSMEM 262 281 6 (Potential).
 FT DOMAIN 283 306 Extracellular (Potential).
 FT TRANSMEM 307 327 7 (Potential).
 FT DOMAIN 328 374 Cytoplasmic (Potential).
 FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
 FT DISULFID 124 204 Potential.
 SQ SEQUENCE 374 AA; 42012 MW; D87A3AC816207319 CRC64;
 Query Match 81.4%; Score 1590; DB 1; Length 374;
 Best Local Similarity 81.0%; Pred. No. 8.4e-101;
 Matches 303; Conservative 27; Mismatches 42; Indels 2; Gaps 1;
 QY 1 MNYPLTLEMD--LENLEDLFWELDRDNDYNDTSLVENHLCPCATEGELPMASFKAVFVPVAY 58
 DB 1 MNSPISLDMGATYNDMDLYKELAYSNSTEIPLODSIFCSTEEGELLTSFKTIFMPVAY 60
 QY 59 SLIFLLGVGNVLVILERHQRSTRSTETFLHLAVADLLVFLPFAVAGSGVGNVLG 118
 DB 61 SLIFLLGMGNLVLVILERHQRSTRSTETFLHLAVADLLVFLPFAVAGSGVGNVLG 120
 QY 119 TFLCKTVIALHKVNFYCSLLILACTAVDRYLAIVHAVYHRRLLSIHTGTIWLGF 178
 DB 121 TFLCKTVIALHKINFYCSLLILACTAVDRYLAIVHAVYHRRLLSIHTGTIWLGF 180
 QY 179 LLALPEILFAKVSQGHNNSLPRCTFSQENAEATRAWFAFRFLYHTGGFLPMLVMAWY 238
 DB 181 LFALPEILFAKVQVPHNNESLPQCFSQENAEATRAWFAFRFLYHTGGFLPMLVMAWY 240
 QY 239 VGVHRLRQARRPQKQKAVRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVENTCKING 298
 DB 241 VGVHRLRQARRPQKQKAVRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVENTCKING 300
 QY 299 SLPAITMCEFLGHAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRS 358
 DB 301 YLSVAITLCEFLGHAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRS 360
 QY 359 SLSESENATSLTTF 372
 DB 361 SLSESENATSLTTF 374

RESULT 5
 O93281 PRELIMINARY; PRT; 392 AA.
 ID O93281 PRELIMINARY; PRT; 392 AA.
 AC O93281; PRELIMINARY; PRT; 392 AA.
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Putative chemokine receptor.
 GN Name=CRLL1;
 OS Gallus Gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98244380; PubMed=9584981;
 RA Gupta S.K., Pillarsetti K., Gray S.L., Stadel J.M.;
 RT "Molecular cloning of a novel chemokine receptor-like gene from early stage chick embryos.";
 RL Biochem. Mol. Biol. Int. 44:673-681(1998).
 DR EMBL: AF029336; AAC23950.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0016493; F: C-C chemokine receptor activity; IEA.
 DR GO: GO:0016494; F: C-X-C chemokine receptor activity; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; F: G-protein coupled receptor protein signalin...; IEA.
 DR InterPro: IPR000355; Chmkin_receptor.

DR	InterPro: IPR001053; CXCL5_receptor.	DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	InterPro: IPR000276; GPCR_Rhodopsn.	DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS; PR00657; CCHEMOKINER.	DR	PRINTS; PR00657; CCHEMOKINER.
DR	PRINTS; PR00564; CXCHMOKINERS.	DR	PRINTS; PR01532; CXCHMOKINER3.
DR	PRINTS; PR00237; GPCRHHODOPNS.	DR	PRINTS; PR00237; GPCRHHODOPNS.
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_1; 1.	DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.	DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor.	KW	G-protein coupled receptor; Receptor; Transmembrane.
SQ	SEQUENCE 392 AA; 44760 MW; 3B5CFCE88366F088 CRC64;	SQ	SEQUENCE 366 AA; 40870 MW; 22AE9D136E09C0F CRC64;
Query Match			
Best Local Similarity 44.4%; Score 866.5; DB 2; Length 392;			
Matches 169; Conservative 57; Mismatches 116; Indels 7; Gaps 3;			
QY	28 NDTSLVENHLCPEATEGLMAS-----EKAVFPVVAYSLIFFLGVGNVLVLILRHQRTR 83	QY	34 ENHLC---PATEGPLMASFKAVFPVVAYSLIFFLGVGNVLVLILRHQRTRSTETFL 90
DB	47 NTPPSLEGYFCFNPSSLWLANQRDPFRKVFIPLAYLLMFVLGTQNALVLILRPFKRSR 106	DB	31 ETYFCTSPPCQDPQSLNFDRTFLFVLSLLFVLGLGNGVAVVLLSQRALSTDTFL 90
QY	84 STETELFLHADVADLLVLEFPAEGSVGVGLTFLCKTVIALHKVNFYCSSLLLACI 143	QY	91 FHLAVADLLVLEFPAEGSVGVGLTFLCKTVIALHKVNFYCSSLLLACIADRYLA 150
DB	107 TTTFENFLHLLTANLALLTTFPSVVSLEAGWVFGTFLCKILSAVHKINFYLHEHAAGLH 166	DB	91 LHLAVADALLVLTPLMVAADAIOHVGSGLCKVAGALFNIFYAGALLACISFDRLS 150
QY	144 ADVRYLAIHVAHYVHRRLLSIHTCGTITMLVGLFLLALPEILFAKVSOQHNNSLPCT 203	QY	151 IVHVAHYHRRLLSIHTCGTITMLVGLFLLALPEILFAKVSOQHNNSL--PRCTFSQEN 208
DB	167 RVDRYLAIVYATYRKARSIHLCTAIWLSLLLTLPDLFMEVWTDENRSI--CY 224	DB	151 IVHATQFYRGPAPARVALTCVAVMGLCLLFAIPDFIFL---SSHNDRLNATHCQYNPQP 207
QY	204 FSOENQAEATHAWFTSRLYHVAAGFLPMLVMGVCYGVVHRLRQAORRQKAVRVAIL 263	QY	209 QAEATHAWFTSRLYHVAAGFLPMLVMGVCYGVVHRLRQAORRQKAVRVAILVTSIF 268
DB	225 FPEAGIHGNVNLATFLYHVGFFPFLVVMCYMAIVRTLQSQRL--QRQKAVRVAIL 283	DB	208 EGRT----ALRVQLVAGFLPLLVMAVCYARILTVL--LVSRGQRRLRAMRLVVVVVAF 262
QY	264 VTSIFPLCWSPHIVIFLDTLARKAVDNTCKLNGSLPVAITWCPEFLGLAHCLNPLMT 323	QY	269 FLCWSPHIVIFLDTLARKAVDNTCKLNGSLPVAITWCPEFLGLAHCLNPLMTFAGVK 328
DB	284 VTGVFLCWSPHIVIFLNTLTKLEAFADCLLEDHLDTAIMVTEAIGFTHCCLNPIIYA 343	DB	263 ALCWTPYHLVVLVDTLMDLGALARNCGRESVDVAKSVTSGMGNHCLNPLLVAFVGVK 322
QY	324 FAGVFRPSDLRLTLKLGCTGSPASLCQFPSSRRSSLSSESNATSLTTF 372	QY	329 FRSDLSRLTLKLGCTG-----PASLCQFPSSRRSSLSSESNAT 367
DB	344 FIGVFRNDFRILHELGCISQETLQELIVETRGCGIESDNTTISLTF 392	DB	323 FRRWVLLMRGLGCPDQGHORQPSA-----SRDSSWSWSETTEAS 362
RESULT 6			
Q867B2	PRELIMINARY; PRT; 366 AA.	Q6GNE2	PRELIMINARY; PRT; 390 AA.
AC	Q867B2;	AC	Q6GNE2;
DT	01-JUN-2003 (TREMBLrel. 24, Created)	DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	01-WAR-2004 (TREMBLrel. 26, Last annotation update)	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	CXC chemokine receptor 3.	DE	LOC443669 protein (Fragment).
GN	Name=cxcr3;	GN	Name=LOC443669;
OS	Capra hircus (Goat).	OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC	Caprinae; Capra.	OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=9925;	OX	NCBI_TaxID=8355;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=22765629; PubMed=12756249; DOI=10.1074/jbc.M300470200;	RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Nagao K., Nollima H., Watanabe F., Chang K.T., Christenson R.K.,	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Sakai S., Imakawa K.	RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RT	"Regulation of Blastocyst Migration, Apposition, and Initial Adhesion	RA	Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RT	by a Chemokine, Interferon (gamma)-inducible Protein 10 kDa (IP-10),	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RT	during Early Gestation."	RA	Stapchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RL	J. Biol. Chem. 278:29048-29056(2003).	RA	Diapchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC	- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
CC	- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
DR	EMBL; AB093893; BC55184.1; ..	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
DR	GO; GO:0016021; C:intracellular to membrane; IEA.	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
DR	GO; GO:0016493; F:C-C chemokine receptor activity; IEA.	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
DR	GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.	RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
DR	GO; GO:0004872; F:receptor-like activity; IEA.	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
DR	InterPro: IPR000355; Chmkin_receptor.	RA	InterPro: IPR000355; Chmkin_receptor.
DR	InterPro: IPR004070; CXCL5_receptor.	RA	InterPro: IPR004070; CXCL5_receptor.

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RN SEQUENCE FROM N.A.
RN TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073571; AAH73571.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F: C-X-C chemokine receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000355; Cmmkine_receptor.
DR InterPro; IPR004070; CXCR3_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01532; CXCR3HKNR3.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
FT NON TER
SQ SEQUENCE 390 AA; 44470 MW; 44294060B6DCA92D CRC64;

* Query Match 32.7%; Score 638.5; DB 2; Length 390;
* Best Local Similarity 39.8%; Pred. No. 7.6e-36;
* Matches 130; Conservative 64; Mismatches 118; Indels 15; Gaps 5;

Qy 49 FKAVFVPAVSLFLGLGVGNVLVILRHQRTRSTETFLPLAVADLLVFLPFAV 108
Db 67 FDRFLPAFYSIFVLGMGNVLVLLQNRWLQSTDFLHLALADLLVVTLPFWA 126

Qy 109 AEGSVGVNLGTFFLTKTIVLHKNVFCSSLLLACIADVRLAIVHAYVHRRLLSIH 168
Db 127 TQAVSGWIFGNVLCKWVASIFKINFYACTELLVCISCDRLSVIYVQLYKHTLVHW 186

Qy 169 TCGTIVLVGLLALPEILFAKVSQGHNNSLPRCTFS-----QENQAETHAWFTS-RPLVH 223
Db 187 SCLLVVCLCIGLSIPDMVYRVTYE-----PRANVTDCQDFGHLDSTWKISLTLVXH 240

Qy 224 VAGFLPMLVMGCVGVVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVFLDT 283
Db 241 IVGFLPLCPFMVVCYTHIIHSLQTHGF-KKQALRVVIAVWVIFFLCWTYPYINVALD 299

Qy 284 LARLKAVDNCKLNGSLPVAITMCEFLGLAHCCINPMLYTFAGVKFRSLRLTLKLGCT 343
Db 300 MNLNLVLPDNCNTDSNIDIALSVTSGLYCYPHSCNLNPLLYAFVGAQPKQLVLLNKLSCI 359

Qy 344 GPASLQCLF---PSWRSSLSSESNAT 367
Db 360 CPQIVKKYIKYNPPAKPSTWSESGDTT 386

RESULT 8
CCR3 HUMAN STANDARD; PRT; 368 AA.
AC P496B2: O15185; Q9P2T4; Q9P2T5;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-3) (CCR-L2) (CD183)

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DE antigen).
GN Name=CXCR3; Synonyms=GPR9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97188912; PubMed=9064356;
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L.,
RA Clark-Lewis I., Baggiolini M., Moser B.;
RT "Chemokine receptor specific for IP10 and mig: structure, function,
RT and expression in activated T-lymphocytes.";
RL J. Exp. Med. 184:963-969(1996).
RN [2]
RN SEQUENCE FROM N.A.
RA Gutierrez J., Varona R., Zaballo A., Lind P., Marquez G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain, Lung, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 5-368 FROM N.A.
RX MEDLINE=96115583; PubMed=8666380;
RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saidi V.V.R.,
RA Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA O'Dowd B.F., Docherty J.M.;
RT "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT Y, and somatostatin receptors.";
RL Genomics 29:335-344(1995).
RN [6]
RN SEQUENCE OF 278-368 FROM N.A., AND VARIANTS GLN-292 AND THR-363.
RX MEDLINE=21040285; PubMed=1196695; DOI=10.1038/sj.gene.6363682;
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Single nucleotide polymorphisms in the coding regions of human CXCR-
RT chemokine receptors CXCR1, CXCR2 and CXCR3.";
RL Genes Immun. 1:330-337(2000).
RN [7]
RN LIGAND BINDING.
RC TISSUE=Fetal astrocytes;
RX MEDLINE=98290735; PubMed=9625760;
RA Cole K.B., Strick C.A., Paradis T.J., Ogborne K.T., Loetscher M.,
RA Gladue R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G.,
RA Neote K.;

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RT "Interferon-inducible T cell alpha chemoattractant (I-TAC): a novel
 RT non-BLR CXCL chemokine with potent activity on activated T cells
 RT through selective high affinity binding to CXCR3.";
 RL J. Exp. Med. 187:2009-2021(1998).
 CC -!- FUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:78-83(2000);
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/650534941_g.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X95876; CAA65126.1; -;
 DR EMBL; Z79783; CAB02143.1; ALT_INIT.
 DR EMBL; AY242128; AAC92295.1; -;
 DR EMBL; BC034403; AAH34403.1; -;
 DR EMBL; U32674; AAC50505.1; -;
 DR EMBL; AB032735; BAA92297.1; -;
 DR EMBL; AB032736; BAA92298.1; -;
 DR GenBank; HGNC:4540; CXCR3.
 DR H-invDB; HIX0016864; -;
 DR MIM; 600894; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . . ; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR InterPro; IPR000355; Chkmln_receptor.
 DR InterPro; IPR004070; GPCR_3_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR01532; CXCHMKINER3.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Antigen; G-protein coupled receptor; Glycoprotein; Polymorphism;
 KW Transmembrane.
 FT DOMAIN 1 53 Extracellular (Potential).
 FT TRANSMEM 54 80 1 (Potential).
 FT DOMAIN 81 89 Cytoplasmic (Potential).
 FT TRANSMEM 90 110 2 (Potential).
 FT DOMAIN 111 125 Extracellular (Potential).
 FT TRANSMEM 126 147 3 (Potential).
 FT DOMAIN 148 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 189 4 (Potential).
 FT DOMAIN 190 212 Extracellular (Potential).
 FT TRANSMEM 213 233 5 (Potential).
 FT DOMAIN 234 255 Cytoplasmic (Potential).
 FT TRANSMEM 256 277 6 (Potential).
 FT DOMAIN 278 298 Extracellular (Potential).
 FT TRANSMEM 299 321 7 (Potential).
 FT DOMAIN 322 368 Cytoplasmic (Potential).
 FT DISULFID 124 203 By similarity.
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 32 32 N-linked (GlcNAc. . .) (Potential).
 FT VARIANT 292 292 R -> Q.
 FT VARIANT 363 363 A -> T.
 FT CONFLICT 75 75 A -> R (in Ref. 2).
 FT SEQUENCE 368 AA; 40659 MW; F08A3B44B2BAD04 CRC64;
 SQ
 Query Match 32.5%; Score 635; DB 1; Length 368;
 Best Local Similarity 40.8%; Pred. No. 1.3e-35;

Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
 QY 11 LENLEDLFWELDRDLDNYNDTSLVENHLCPATEGLPMASFKAVFPVAVSLIFLLGVGNV 70
 DB 20 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLGLLNG 72
 QY 71 LVLVILHRHQRTRSTETFLFLHVLAVADLLVFLPFAVAEGSVGVWLTGFLCKTIVLHK 130
 DB 73 AVAAVLLSRRTALSTDTFLFLHVLAVADLLVLTLPMAVDAVQWVFGSLCKVAGALFN 132
 QY 131 VNFYCSLLACIAVDRLAIIVHVAHYVRHRELLSIHITCGTIWLGVFLALPEILFAKV 190
 DB 133 INFYAGALLACISFDRLINIVHATQLYRRGPAPRVTLTCLAVMGICLLFALPDPFL-- 190
 QY 191 SOGHNNSL--PRCTFSQENQAEHTAMFTSRFLYHVAGFLPMLVMGVCYGVVHRLROA 248
 DB 191 -SAHDERLNLNATHCOYNPQVGR-----ALRVQLVAGVFLPLLVNAYCAHILAVL-LV 244
 QY 249 QRRPQOKAVRVAIIIVTSIFFLCWSPHYVIFDLTLARLKAVDNTCKLNSLPVATTMCE 308
 DB 245 SRGQRRLRAMRLVVVVVAFALCWTPTPHLVLDVILMDLGALARNCGRESRVDAKSVTS 304
 QY 309 FLGLAHCCINPMLYTFAGVKFRSRLITKLGCTGPASLCOFPSPWRR--SSLSESENAT 367
 DB 305 GLGYMHCCINPLLYAFVGVKFRERMMWMLLRLLGCPNQRLQRPSSRRDSSWSETSEAS 364
 RESULT 9
 Q7Z710 PRELIMINARY; PRT; 415 AA.
 ID Q7Z710
 AC Q7Z710
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CXCL chemokine receptor transcript variant B.
 GN Name=GPR9;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RX MEDLINE=22666871; PubMed=12782716;
 RA Laesagni L., Francalanci M., Annunziato F., Lazzeri E., Giannini S.,
 RA Cosmi L., Sagrinati C., Mazzinghi B., Orlando C., Maggi E., Marra F.,
 RA Romagnani S., Serio M., Romagnani P.;
 RA "An alternatively spliced variant of CXCR3 mediates the inhibition of
 RT endothelial cell growth induced by IP-10, Mig, and I-TAC, and acts as
 RT functional receptor for platelet factor 4.";
 RL J. Exp. Med. 197;1537-1549(2003).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC EMBL; AF469635; AAP55851.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 415 AA; 45522 MW; 325C8A65982A43C4 CRC64;
 Query Match 32.5%; Score 635; DB 2; Length 415;
 Best Local Similarity 40.8%; Pred. No. 1.4e-35;
 Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
 QY 11 LENLEDLFWELDRDLDNYNDTSLVENHLCPATEGLPMASFKAVFPVAVSLIFLLGVGNV 70
 DB 67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLGLLNG 119
 QY 71 LVLVILHRHQRTRSTETFLFLHVLAVADLLVFLPFAVAEGSVGVWLTGFLCKTIVLHK 130

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Db 120 A V A V L L S R R T A L S T D T F L L H L A V A D T L L V L T L P L W A V D A A V Q M V F G S G L C K V A G A L F N 179
QY 131 V N F V C S S L L A C T A V D R Y L A I V H A V H A Y R H R L L S I H I T G T T W L V G F L L A L P E I L F A K V 190
Db 180 I N F Y A G A L L A C I S F D R I L N I V H A T Q Y R G P P A R V T L T C L A V N G L C L L F A L P D F I P L -- 237
QY 191 S Q G H H N S L -- P R C T F S Q E N Q A E T H A W F T S R F L Y H V A G F L L P M L V M G W C Y G V V H R L R Q A 248
Db 238 - S A H D E R L N A T H C Q Y N F P Q V G R T - - - - A L R V L Q L V A G F L L P L L V M A Y C Y A H I L A V L - L V 291
QY 249 Q R A P O R Q A V R V A I L V T S I F F L C W S P H I V I F L D T L A R L K A V D N T C K L N G S L P V A T M C E 308
Db 292 S R G O R R L A R N L V V V V V V A F A L C W T P Y H L V L V D I L M D L G A L A R N C R E S R V D V A K S V T S 351
QY 309 F L G L A H C L L N P M L Y T F A G V F R S D L S R L L T K G C T G P A S C O L F P P S W R R - S S L S E S E N A T 367
Db 352 G L G V M H C L L A P L L Y A F V G V F R E R M W M L L R L G C P N O R G L O R Q P S S R R D S S W S E T S E A S 411

RESULT 10
Q9QWN6 PRELIMINARY; PRT; 367 AA.
AC Q9QWN6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Interferon-inducible protein 10 receptor.
GN Name=Cxcr3; Synonyms=MCXCR3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=99009219; PubMed=9790904; DOI=10.1006/bbrc.1998.9404;
RA Tamari M., Tomimaga Y., Yatsunami K., Narumi S.;
RT "Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its specific expression in lymphoid organs.";
RL Biochem. Biophys. Res. Commun. 251:41-48(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB003174; BAA34045.1; -.
DR PIR; JEO349; JEO349.
DR MGD; MGI:1277207; Cxcr3.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR004070; CXC 3 receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CXCHEMOKINER.
DR PRINTS; PR01532; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41017 MW; EF0348A8358AD951 CRC64;

Query Match 31.5%; Score 615; DB 2; Length 367;
Best Local Similarity 38.8%; Pred. No. 2.9e-34;
Matches 134; Conservative 58; Mismatches 139; Indels 14; Gaps 6;

QY 28 N D T S L V E N H L C P A T E G P L M A S E K A V F P V A Y S F I L L G V I G N V L V L E R H R O T S S T E 87
Db 32 N E S D F S D S P C P Q - - - D F S I N F O R T F A L Y S L F L L G L I G N G A V A A V L L S Q R T A L S D T 88
QY 88 T E L F L A V A D L L V I L P F A V A E G S V G W L G T F L C K T V I A L H K V N F Y C S L L L A C I A V D R 147
Db 89 T F L L H L A V A D V L L V T L P L W A V D A A V Q M V F G L C K V A G A L F N I N F A G F L A C I S F D R 148
QY 148 Y L A I V H A V H A Y R H R L L S I H I T C G T I W L V G F L L A L P E I L F A K V S Q G H H N S L P R C T F S Q E 207

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Db 149 Y L S I V H A T Q I Y R R D P R V R V A L T C I V V W G L C L L F A L P D F I Y L S A N Y D O R L N A - T H C Q N F P 207
QY 208 N Q A E T H A W F T S R F L Y H V A G F L L P M L V M G W C Y G V V H R L R Q A O R R P O K A V R V A I L V T S I 267
Db 208 Q V G R T - - - - A L R V L Q L V A G F L L P L L V M A Y C Y A H I L A V L - L V S R G O R R F R A M R L V V V V A A 262
QY 268 F P L C W S P H I V I F L D T L A R L K A V D N T C K L N G S L P V A T M C E F L G L A H C L L N P M L Y T F A G V 327
Db 263 F A V C W T P Y H L V L V D I L M D V G L A R N C R E S H V D V A K S V T S G M G Y M H C L L P L L Y A F V G V 322
QY 328 K F R S D L S R L L T K G C T - - - G P A S C O L F P P S W R R S S L S E S E N A T S L 369
Db 323 K F R E Q W M L F T L R G S D Q R G P O R - - Q P S S R R E S S W S E T E A S Y L 365

RESULT 11
CCR3_MOUSE STANDARD; PRT; 367 AA.
AC CCR3_MOUSE;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-3) (CXCR-3).
GN Name=Cxcr3; Synonyms=Cmkar3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818636; PubMed=9653165; DOI=10.1073/pnas.95.14.8205;
RA Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Hedrick J., Zlotnik A.;
RT "The CC chemokine 6CKine binds the CXCR chemokine receptor CXCR3.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
CC -1- FUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC (By similarity). Binds to SCYB1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC EMBL; AF045146; AAC40163.1; -.
DR MGD; MGI:1277207; Cxcr3.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR004070; CXC 3 receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01532; CXCHEMOKINER3.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 52 Extracellular (Potential).
FT TRANSMEM 53 79 1 (Potential).
FT DOMAIN 80 88 Cytoplasmic (Potential).
FT TRANSMEM 89 109 2 (Potential).
FT DOMAIN 110 124 Extracellular (Potential).
FT TRANSMEM 125 146 3 (Potential).
FT DOMAIN 147 168 Cytoplasmic (Potential).
FT TRANSMEM 169 188 4 (Potential).
FT DOMAIN 189 211 Extracellular (Potential).
FT TRANSMEM 212 232 5 (Potential).
FT DOMAIN 233 254 Cytoplasmic (Potential).
FT TRANSMEM 255 276 6 (Potential).
FT TRANSMEM 277 297 Extracellular (Potential).
FT TRANSMEM 298 320 7 (Potential).

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SQ SEQUENCE 374 AA; 41113 MW; DEBD92B366776A0D CRC64;
 Query Match 31.1%; Score 607; DB 2; Length 374;
 Best Local Similarity 40.2%; Pred. No. 1e-33;
 Matches 137; Conservative 55; Mismatches 123; Indels 26; Gaps 9;
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 DB 10 LDEADLLPMGLNDTSELDNPPRPAATAPTCLAPSQSFHRVFLPVVYGLVCLLGFAGNGL 69
 QY 72 LVILERHQRTRSTETFLHVAADLLVFLPFAVAGSVGWLTGFLCKTVIALHKV 131
 DB 70 ILVLTCTKRTSSDDYLMHLAADDLLVLTMPFAVAGSATEWVFNVLCCLVNFTFTV 129
 QY 132 NFYCSSLACIAVDRLAIVAHVAYRHRRLLSIHITCGTIVLGVFLALPEILPAKV- 190
 DB 130 NLASSILLACISIERVLAIVRATKDKVRKPKATKYTCGAVWALSLLAMPDLVSHVY 189
 QY 191 ---SQGHH--NNSLPRTCFSQENQAETHAWFTS--RFLYHVAGFLLPMLVGMWCVGVVHR 244
 DB 190 IAPLSGHOLCEHVYP-----ESASELWRTSLRALHHLVAFALPGIVIVFCVMVIRT 241
 QY 245 LRAQRPRQKAVRVAILVTSIFFLCWSPHYHIVFDLTARLKAVDNT-CKLNGSLPVA 303
 DB 242 LSQLNHH-EKKALKVVVAIAAFAFFVCWLPYNNVVTLLDTRMLDVAVNSDCEMEQRLGVA 300
 QY 304 ITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTG 344
 DB 301 VAVTEGVGFSHCCPIPVYAFVGVKKENLARLNGCKACVG 341

RESULT 14

Q8HZN4 PRELIMINARY; PRT; 355 AA.
 AC Q8HZN4
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 8 receptor B CXCR2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecus.
 OX NCBI_TaxID=60710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl B.,
 RA Baldwin J.J., Auld D.S.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF540793; AANL7319.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004918; F:interleukin-8 receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000057; IL8B_receptor.
 DR InterPro; IPR000174; IL8B_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G PROTEIN RECEPT F1_1; 1.
 DR PROSITE; PS00237; G PROTEIN RECEPT F1_2; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPT F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 355 AA; 40381 MW; D464957687BBFEBF CRC64;
 Query Match 31.0%; Score 606; DB 2; Length 355;
 Best Local Similarity 39.0%; Pred. No. 1.2e-33;
 Matches 142; Conservative 54; Mismatches 156; Indels 12; Gaps 8;

RESULT 15

Q8HZN8 PRELIMINARY; PRT; 355 AA.
 AC Q8HZN8
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 8 receptor B CXCR2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl B.,
 RA Baldwin J.J., Auld D.S.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF540789; AANL7315.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004918; F:interleukin-8 receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000057; IL8B_receptor.
 DR InterPro; IPR000174; IL8B_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G PROTEIN RECEPT F1_1; 1.
 DR PROSITE; PS00237; G PROTEIN RECEPT F1_2; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPT F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 355 AA; 40122 MW; 809AB63ADA6A42C6 CRC64;
 Query Match 30.8%; Score 601.5; DB 2; Length 355;
 Best Local Similarity 38.6%; Pred. No. 2.4e-33;
 Matches 141; Conservative 57; Mismatches 154; Indels 13; Gaps 8;
 QY 9 MDLENLEDLFWELDRDNDYNTSLVENHLCPCATE-GPLMASFKAVFVPVAVSLIFLLGVI 67

Db 1 MESDSFED-FWKGEDLSNYSSTLPPFLDADCEPESLEINKYFVYIYALVFLLSLL 59
QY 68 GNVLVILRHRQTRSTETFLPHLAVADLLVFLPFAVAGSGVGLGTFELCKTVIA 127
Db 60 GNSLWMLVILYSRVGRSVTDVYLLNLALADLLFALTLPWAASKVNGWIFGTFLCKVSL 119
QY 128 LHKVNFYCSSLILLACIADVRLAIYHAYHAYHRRLLSIHITCGTIWLVGFILLALPEILF 187
Db 120 LKEVNFYSGILLACISVDRYLAIVHATRTLTKRYL-VKFCISIWGLSLLALPVLFF 178
QY 188 AKYSQGHNNLSLPRCTFSQENQAEHAW-FTSRFLYHVAGFLPMLVMGWCYGVVHRLR 246
Db 179 RRTV--YSSNVSPACYEDMGN--NTANRWMLRLILPOSGFIPELLIMLFCYGTTLTLF 234
QY 247 QAQRPPQOKAVRVAILVTSIFFLCWSPHYHIVFLDTLARLKAVDNTCKLNGSLPVAITM 306
Db 235 KA-HMGQKHAMRVIFAVVLIFFLCWLPYNVLLADTLMTQVIOETCERRNHIDRALDA 293
QY 307 CEFGLAHCCINPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLPFSWRSSLSSENA 366
Db 294 TEILGILHSCINPLIYAFIQKFRHGILLKILAIHGLISKDSL----PKDSRPSFVGSSG 349
QY 367 TSLTT 371
Db 350 HTSTT 354

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OM protein - protein search, using sw model

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(without alignments)
661.177 Million cell updates/sec

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Perfect score: 1953
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/prodata/1/iaa/PCUS COMB.pcp.*
6: /cgn2_6/prodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1953	100.0	372	1	US-08-076-093A-6
3	1953	100.0	372	1	US-08-701-265-6
4	1953	100.0	372	2	US-08-284-586-6
5	1953	100.0	372	2	US-08-805-478-6
6	1953	100.0	372	2	US-08-802-627A-6
7	1953	100.0	372	2	US-08-801-238-6
8	1953	100.0	372	2	US-08-801-228-6
9	1953	100.0	372	3	US-09-104-296-6
10	1953	100.0	372	3	US-08-982-493-8
11	1953	100.0	372	4	US-09-170-496D-66
12	1953	100.0	378	4	US-09-949-016-10255
13	1947	99.7	372	4	US-09-170-496D-200
14	1635	83.7	374	3	US-08-982-493-6
15	635	32.5	368	3	US-08-709-838-2
16	635	32.5	368	3	US-08-829-839-2
17	635	32.5	368	4	US-09-170-496D-20
18	635	32.5	368	4	US-09-624-594-2
19	635	32.5	368	4	US-09-607-156-2
20	632	32.4	368	4	US-09-170-496D-174
21	601.5	30.8	355	1	US-07-759-568-1
22	601.5	30.8	355	1	US-08-450-393A-8
23	601.5	30.8	355	2	US-08-390-000A-5
24	601.5	30.8	355	3	US-08-446-669-8
25	601.5	30.8	355	4	US-09-625-573-8
26	601.5	30.8	355	5	PCT-US95-00476-8
27	601.5	30.8	360	1	US-08-202-056-7

28 601.5 30.8 360 4 US-09-409-778-4 Sequence 4, Appli
29 596 30.5 358 1 US-08-153-848-19 Sequence 19, Appl
30 596 30.5 358 3 US-09-299-843A-19 Sequence 19, Appl
31 596 30.5 358 3 US-09-088-337B-19 Sequence 19, Appl
32 596 30.5 358 5 PCT-US93-11153-19 Sequence 19, Appl
33 596 30.5 378 1 US-08-153-848-15 Sequence 15, Appl
34 596 30.5 378 3 US-09-299-843A-15 Sequence 15, Appl
35 596 30.5 378 3 US-09-251-545-1 Sequence 1, Appl
36 596 30.5 378 3 US-09-088-337B-15 Sequence 15, Appl
37 596 30.5 378 4 US-09-170-496D-74 Sequence 74, Appl
38 596 30.5 378 5 PCT-US93-11153-15 Sequence 15, Appl
39 596 30.5 410 1 US-08-153-848-7 Sequence 7, Appl
40 596 30.5 410 3 US-09-299-843A-7 Sequence 7, Appl
41 596 30.5 410 3 US-09-088-337B-7 Sequence 7, Appl
42 596 30.5 410 5 PCT-US93-11153-7 Sequence 7, Appl
43 591 30.3 378 4 US-09-170-496D-204 Sequence 204, App
44 574 29.4 378 1 US-08-383-750-2 Sequence 2, Appli
45 574 29.4 378 1 US-08-383-751A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-202-056-5
; Sequence 5, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-202-056-5

Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNYPLTLEMDLENLEDFWELDRDNYNDTSLVENHLCPATEGFLMASFKAVFVPVAYSL 60

Db 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASPKAFVFPVAYS 60
Qy 61 IFLLGVGNVLVILERHRTSSSTETFLFLAVADLLAVFLLPFAVAEGSVGWLGTF 120
Db 61 IFLLGVGNVLVILERHRTSSSTETFLFLAVADLLAVFLLPFAVAEGSVGWLGTF 120
Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
Db 121 LCKTVIALHKVNFYCSSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
Qy 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYV 240
Db 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYV 240
Qy 241 VVHRLQAORRQORQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAORRQORQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
Db 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 2

US-08-076-093A-6
; Sequence 6, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid

; TOPOLOGY: Linear
US-08-076-093A-6
Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASPKAFVFPVAYS 60
Db 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASPKAFVFPVAYS 60
Qy 61 IFLLGVGNVLVILERHRTSSSTETFLFLAVADLLAVFLLPFAVAEGSVGWLGTF 120
Db 61 IFLLGVGNVLVILERHRTSSSTETFLFLAVADLLAVFLLPFAVAEGSVGWLGTF 120
Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
Db 121 LCKTVIALHKVNFYCSSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
Qy 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYV 240
Db 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYV 240
Qy 241 VVHRLQAORRQORQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAORRQORQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
Db 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 3

US-08-701-265-6
; Sequence 6, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B

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;
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-701-265-6

Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLYNNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
Db 1 MNYPLTLEMDLENLEDFWELDRDLYNNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60

QY 61 IFLGVIGNVLVLILRHQRTRSTETFLFLAVADLLLVFILPFAVAGSVGWLGT 120
Db 61 IFLGVIGNVLVLILRHQRTRSTETFLFLAVADLLLVFILPFAVAGSVGWLGT 120

QY 121 LCKTVIALHKVNFYCSLLIACIAVDRYLAIHVAVHAYHRRLLSIHITCGTIWL 180
Db 121 LCKTVIALHKVNFYCSLLIACIAVDRYLAIHVAVHAYHRRLLSIHITCGTIWL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHAGVFLPMLVMG 240
Db 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHAGVFLPMLVMG 240

QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPHYHIVFLDTLARKAVDNTCK 300
Db 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPHYHIVFLDTLARKAVDNTCK 300

QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLP 360
Db 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLP 360

QY 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 4
US-08-284-586-6
; Sequence 6, Application US/08284586
; Patent No. 5840856
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-284-586-6

Query Match 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLYNNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
Db 1 MNYPLTLEMDLENLEDFWELDRDLYNNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60

QY 61 IFLGVIGNVLVLILRHQRTRSTETFLFLAVADLLLVFILPFAVAGSVGWLGT 120
Db 61 IFLGVIGNVLVLILRHQRTRSTETFLFLAVADLLLVFILPFAVAGSVGWLGT 120

QY 121 LCKTVIALHKVNFYCSLLIACIAVDRYLAIHVAVHAYHRRLLSIHITCGTIWL 180
Db 121 LCKTVIALHKVNFYCSLLIACIAVDRYLAIHVAVHAYHRRLLSIHITCGTIWL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHAGVFLPMLVMG 240
Db 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHAGVFLPMLVMG 240

QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPHYHIVFLDTLARKAVDNTCK 300
Db 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPHYHIVFLDTLARKAVDNTCK 300

QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLP 360
Db 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLP 360

QY 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 5
US-08-805-478-6
; Sequence 6, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```

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;
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-805-478-6
;
; Query Match 100.0%; Score 1953; DB 2; Length 372;
; Best Local Similarity 100.0%; Pred. No. 8.7e-176;
; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
; DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
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; QY 61 IFLLGVGNVLVLILRHRQTRSSSTETFLFLAVADLLLVFILPFAVAGSVGVVLGTF 120
; DB 61 IFLLGVGNVLVLILRHRQTRSSSTETFLFLAVADLLLVFILPFAVAGSVGVVLGTF 120
;
; QY 121 LCKTVIALHKVNFYCSSLILACIAVDRLAIHVAVHAYRHRLLSHITCGTIWLVGFLL 180
; DB 121 LCKTVIALHKVNFYCSSLILACIAVDRLAIHVAVHAYRHRLLSHITCGTIWLVGFLL 180
;
; QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
; DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
;
; QY 241 VVHRLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
; DB 241 VVHRLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
;
; QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLFPSWRRSSL 360
; DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLFPSWRRSSL 360
;
; QY 361 SESENATSLTTF 372
; DB 361 SESENATSLTTF 372

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RESULT 6

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US-802-627A-6
; Sequence 6, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James

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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,627A
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-802-627A-6
;
; Query Match 100.0%; Score 1953; DB 2; Length 372;
; Best Local Similarity 100.0%; Pred. No. 8.7e-176;
; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
; DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
;
; QY 61 IFLLGVGNVLVLILRHRQTRSSSTETFLFLAVADLLLVFILPFAVAGSVGVVLGTF 120
; DB 61 IFLLGVGNVLVLILRHRQTRSSSTETFLFLAVADLLLVFILPFAVAGSVGVVLGTF 120
;
; QY 121 LCKTVIALHKVNFYCSSLILACIAVDRLAIHVAVHAYRHRLLSHITCGTIWLVGFLL 180
; DB 121 LCKTVIALHKVNFYCSSLILACIAVDRLAIHVAVHAYRHRLLSHITCGTIWLVGFLL 180
;
; QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
; DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
;
; QY 241 VVHRLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
; DB 241 VVHRLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
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; QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLFPSWRRSSL 360
; DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLFPSWRRSSL 360
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; QY 361 SESENATSLTTF 372
; DB 361 SESENATSLTTF 372

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Db          361 SESENATSLTTF 372
RESULT 7
US-08-801-238-6
; Sequence 6, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-238-6
Query Match          100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MNYPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
Db      1 MNYPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
QY      61 IFLGVIGNVLVILERHRTSRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
Db      61 IFLGVIGNVLVILERHRTSRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
QY      121 LCKTVIALHKVNFYCSSLLACIADRYLAIYHVAHYHRRLLSIHITCGTIWLVGFL 180
Db      121 LCKTVIALHKVNFYCSSLLACIADRYLAIYHVAHYHRRLLSIHITCGTIWLVGFL 180
QY      181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAEHTAMFTSRFLYHAGVLLPMLVMGCVVG 240
Db      181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAEHTAMFTSRFLYHAGVLLPMLVMGCVVG 240
QY      241 VVHLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKNGSL 300
Db          361 SESENATSLTTF 372
RESULT 8
US-08-801-228-6
; Sequence 6, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-228-6
Query Match          100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MNYPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
Db      1 MNYPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
QY      61 IFLGVIGNVLVILERHRTSRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
Db      61 IFLGVIGNVLVILERHRTSRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
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Qy 121 LCKTVIALHKVNFYCSSLLIACIAVDRLAIYHVAHVAYRHRLLSIHITCGTIWLVGFLL 180
Db 121 LCKTVIALHKVNFYCSSLLIACIAVDRLAIYHVAHVAYRHRLLSIHITCGTIWLVGFLL 180
Qy 181 ALPEILFAKVSQGHNNSLPRCTFSEQNOAETHAWFTSRFLYHVAAGFLPMLVMGWCYVG 240
Db 181 ALPEILFAKVSQGHNNSLPRCTFSEQNOAETHAWFTSRFLYHVAAGFLPMLVMGWCYVG 240
Qy 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Db 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 9

US-09-104-296-6
; Sequence 6, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PP4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,296
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-09-104-296-6

Query Match 100.0%; Score 1953; DB 3; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNYPLTLEMDLENLEDLFWELDRNLNYNDTSLVENHLCPATEGPLMASFKAVFPVAYSL 60
Db 1 MNYPLTLEMDLENLEDLFWELDRNLNYNDTSLVENHLCPATEGPLMASFKAVFPVAYSL 60
Qy 61 IFELGVIGNVLVILERHRQTRSTETFLFHLAVADLLLVILPFAVAEGSVGVLTGF 120
Db 61 IFELGVIGNVLVILERHRQTRSTETFLFHLAVADLLLVILPFAVAEGSVGVLTGF 120
Qy 121 LCKTVIALHKVNFYCSSLLIACIAVDRLAIYHVAHVAYRHRLLSIHITCGTIWLVGFLL 180
Db 121 LCKTVIALHKVNFYCSSLLIACIAVDRLAIYHVAHVAYRHRLLSIHITCGTIWLVGFLL 180
Qy 181 ALPEILFAKVSQGHNNSLPRCTFSEQNOAETHAWFTSRFLYHVAAGFLPMLVMGWCYVG 240
Db 181 ALPEILFAKVSQGHNNSLPRCTFSEQNOAETHAWFTSRFLYHVAAGFLPMLVMGWCYVG 240
Qy 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Db 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 10

US-08-982-493-8
; Sequence 8, Application US/08982493
; Patent No. 6110695
; GENERAL INFORMATION:
; APPLICANT: Gunn, Michael D
; APPLICANT: Williams, Lewis T
; APPLICANT: Cyster, Jason G
; TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /
; TITLE OF INVENTION: Receptor Interactions
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,493
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCSFT98-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-982-493-8

Query Match
Best Local Similarity 100.0%; Score 1953; DB 3; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
QY 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLLTKLGGTGPASLCQLPFSWRRSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLLTKLGGTGPASLCQLPFSWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 11
US-09-170-496D-66
; Sequence 66, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 66
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-66

Query Match
Best Local Similarity 100.0%; Score 1953; DB 4; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
QY 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180

MOLECULE TYPE: protein
US-08-982-493-8

Query Match
Best Local Similarity 100.0%; Score 1953; DB 3; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
QY 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLLTKLGGTGPASLCQLPFSWRRSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLLTKLGGTGPASLCQLPFSWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 12
US-09-949-016-10255
; Sequence 10255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10255
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10255

Query Match
Best Local Similarity 100.0%; Score 1953; DB 4; Length 378;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 7 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 66
QY 61 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 67 IFLLGVIGNVLVLILERHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 126
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
DB 127 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 186
QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 187 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 246
QY 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 247 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 306
QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLLTKLGGTGPASLCQLPFSWRRSSL 360
DB 307 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLLTKLGGTGPASLCQLPFSWRRSSL 366
QY 361 SESENATSLTTF 372
DB 367 SESENATSLTTF 378

RESULT 13
US-09-170-496D-200
; Sequence 200, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170.496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-200

Query Match 99.7%; Score 1947; DB 4; Length 372;
Best Local Similarity 99.7%; Pred. No. 3.2e-175;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDNDYNDTSLVENHLCPCATEGFLMASFKAVFVPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDNDYNDTSLVENHLCPCATEGFLMASFKAVFVPVAYSL 60
QY 61 IFGLGVIGNVLVLILRHRQTRSSSTETFLHLAVADLLLVFILPFAVAEGSVGWVLGTF 120
DB 61 IFGLGVIGNVLVLILRHRQTRSSSTETFLHLAVADLLLVFILPFAVAEGSVGWVLGTF 120
QY 121 LCKTVIALHKVNFVCSLLACIADRYLAIVHAYRHRRLISIHITCGTILWVGFL 180
DB 121 LCKTVIALHKVNFVCSLLACIADRYLAIVHAYRHRRLISIHITCGTILWVGFL 180
QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVGMWCYVG 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVGMWCYVG 240
QY 241 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNSL 300
DB 241 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNSL 300
QY 301 PVAITMCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPSSWRSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPSSWRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 14
US-08-982-493-6
; Sequence 6, Application US/08982493
; Patent No. 6110695
; GENERAL INFORMATION:
; APPLICANT: Gunn, Michael D
; APPLICANT: Williams, Lewis T
; APPLICANT: Cyster, Jason G
; TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /
; TITLE OF INVENTION: Receptor Interactions
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA

ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,493
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCSFT98-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-982-493-6

Query Match 83.7%; Score 1635; DB 3; Length 374;
Best Local Similarity 82.9%; Pred. No. 7.5e-146;
Matches 310; Conservative 29; Mismatches 33; Indels 2; Gaps 1;
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DB 1 MNYPLTLEMDGSIYNNDDLYKELAFYSNSTEIPLQDSNFCSTVEGFLLSFKAVFVPVAY 60
QY 59 SLIFLGVIGNVLVLILRHRQTRSSSTETFLHLAVADLLLVFILPFAVAEGSVGWVLG 118
DB 61 SLIFLGVIGNVLVLILRHRQTRSSSTETFLHLAVADLLLVFILPFAVAEGSVGWVLG 120
QY 119 TFLCKTVIALHKVNFVCSLLACIADRYLAIVHAYRHRRLISIHITCGTILWVG 178
DB 121 TFLCKTVIALHKVNFVCSLLACIADRYLAIVHAYRHRRLISIHITCGTILWLAGF 180
QY 179 LLALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVGMWCY 238
DB 181 LFALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVGMWCY 240
QY 239 VGVVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG 298
DB 241 VGVVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLSG 300
QY 299 SLFVAITMCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPSSWRS 358
DB 301 YLSVAITLCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPNWRKS 360
QY 359 SLSESENATSLTTF 372
DB 361 SLSESENATSLTTF 374

RESULT 15
US-08-709-838-2
; Sequence 2, Application US/08709838
; Patent No. 6140064
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA

Search completed: August 29, 2005, 23:58:34
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:51:16 ; Search time 164 Seconds
(without alignments)
891.272 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MMYPTLEMDLENLEDFWE.....PSWRRSSLSSESNATSLTTF 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1953	100.0	372	14	US-10-251-385-66
3	1953	100.0	372	14	US-10-225-567A-60
4	1953	100.0	372	14	US-10-239-423-80
5	1953	100.0	372	15	US-10-666-689-6
6	1953	100.0	378	15	US-10-276-774-2243
7	1947	99.7	372	14	US-10-251-385-200
8	1938.5	99.3	371	20	US-11-021-951-154
9	635	32.5	368	14	US-10-251-385-20
10	635	32.5	368	14	US-10-225-567A-74
11	635	32.5	368	14	US-10-345-680-59

12	635	32.5	368	14	US-10-251-686-2
13	635	32.5	368	14	US-10-239-423-78
14	635	32.5	368	15	US-10-411-284-4
15	635	32.5	368	15	US-10-295-027-752
16	635	32.5	368	16	US-10-733-878-304
17	635	32.5	368	17	US-10-949-135-34
18	635	32.5	368	17	US-10-510-121-2
19	635	32.5	368	20	US-11-021-951-155
20	635	32.5	415	15	US-10-411-284-2
21	632	32.4	368	14	US-10-251-385-174
22	624.5	32.0	472	14	US-10-106-698-6402
23	621	31.8	415	16	US-10-733-878-517
24	604	30.9	355	14	US-10-237-563-36
25	601.5	30.8	354	15	US-10-411-284-11
26	601.5	30.8	355	10	US-09-893-512-10
27	601.5	30.8	355	14	US-10-237-563-27
28	601.5	30.8	355	14	US-10-237-563-28
29	601.5	30.8	355	16	US-10-791-592-8
30	601.5	30.8	355	16	US-10-791-166-8
31	601.5	30.8	355	17	US-10-799-736-10
32	601.5	30.8	360	13	US-10-087-192-882
33	601.5	30.8	360	14	US-10-099-007A-16
34	601.5	30.8	360	14	US-10-225-567A-386
35	601.5	30.8	360	14	US-10-239-423-77
36	601.5	30.8	360	14	US-10-101-148-4
37	601.5	30.8	360	17	US-10-690-880-25
38	601.5	30.8	399	15	US-10-334-143-7
39	601.5	30.8	399	15	US-10-276-774-2394
40	600.5	30.7	355	14	US-10-237-563-29
41	596.5	30.5	355	14	US-10-237-563-30
42	596.5	30.5	355	14	US-10-237-563-34
43	596	30.5	378	14	US-10-251-385-74
44	596	30.5	378	14	US-10-225-567A-68
45	596	30.5	378	14	US-10-239-423-70

ALIGNMENTS

RESULT 1
US-09-104-063-6
; Sequence 6, Application US/09104063
; Patent No. US20020168356A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PE4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,063
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-Aug-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993

Sequence 2, Appli
Sequence 78, Appli
Sequence 4, Appli
Sequence 752, App
Sequence 304, App
Sequence 34, Appli
Sequence 2, Appli
Sequence 155, App
Sequence 174, App
Sequence 6402, Ap
Sequence 517, App
Sequence 36, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 882, App
Sequence 16, Appli
Sequence 386, App
Sequence 77, Appli
Sequence 4, Appli
Sequence 25, Appli
Sequence 7, Appli
Sequence 2394, Ap
Sequence 29, Appli
Sequence 30, Appli
Sequence 34, Appli
Sequence 74, Appli
Sequence 68, Appli
Sequence 70, Appli

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: F0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-104-063-6

Query Match 100.0%; Score 1953; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
DB 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120
DB 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240

QY 241 VVHLRQAORRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 241 VVHLRQAORRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 2
US-10-251-385-66
; Sequence 66, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-104-063-6

Query Match 100.0%; Score 1953; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
DB 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120
DB 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240

QY 241 VVHLRQAORRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 241 VVHLRQAORRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 2
US-10-251-385-66
; Sequence 66, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-251-385-66

Query Match 100.0%; Score 1953; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
DB 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120
DB 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240

QY 241 VVHLRQAORRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 241 VVHLRQAORRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 3
US-10-225-567A-60
; Sequence 60, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-60

Query Match 100.0%; Score 1953; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
DB 1 MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120
DB 61 IFLLGVIGNVLVLILERHRQTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHYRHRLLSHITCGTIWLVGFL 180
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QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 4
US-10-239-423-80
; Sequence 80, Application US/10239423
; Publication No. US2003018689A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMAN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
; TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 02217us
; CURRENT APPLICATION NUMBER: US/10/239, 423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 80
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-80
Query Match 100.0%; Score 1953; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0;
QY 1 MNPPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATGCPMLMASFKAVFVPVAVSL 60
DB 1 MNPPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATGCPMLMASFKAVFVPVAVSL 60
QY 61 IFLLGVGNVLVLILHRQTRSSSTETFLHVAADLLVLPFAVAEGSVGWVLTGF 120
DB 61 IFLLGVGNVLVLILHRQTRSSSTETFLHVAADLLVLPFAVAEGSVGWVLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIHVHAYVHRRLLSIHITCGTILVGVFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIHVHAYVHRRLLSIHITCGTILVGVFL 180
QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 5
US-10-666-689-6
; Sequence 6, Application US/10666689
; Publication No. US20040037830A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Human FF4A Receptors, Nucleic Acid Encoding and
; TITLE OF INVENTION: Antibodies Binding Thereto
; FILE REFERENCE: P0706P2C2D2C1
; CURRENT APPLICATION NUMBER: US/10/666,689
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 09/104,063
; PRIOR FILING DATE: 1988-06-24
; PRIOR APPLICATION NUMBER: US 08/701,265
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/664,228
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/076,093
; PRIOR FILING DATE: 1993-06-11
; PRIOR APPLICATION NUMBER: US 07/810,782
; PRIOR FILING DATE: 1991-12-19
; PRIOR APPLICATION NUMBER: US 07/677,211
; PRIOR FILING DATE: 1991-03-29
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-666-689-6
Query Match 100.0%; Score 1953; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0;
QY 1 MNPPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATGCPMLMASFKAVFVPVAVSL 60
DB 1 MNPPLTLEMDLENLEDFWELDRDLDNYDTSLVENHLCPCATGCPMLMASFKAVFVPVAVSL 60
QY 61 IFLLGVGNVLVLILHRQTRSSSTETFLHVAADLLVLPFAVAEGSVGWVLTGF 120
DB 61 IFLLGVGNVLVLILHRQTRSSSTETFLHVAADLLVLPFAVAEGSVGWVLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIHVHAYVHRRLLSIHITCGTILVGVFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIHVHAYVHRRLLSIHITCGTILVGVFL 180
QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 6
US-10-276-774-2243
; Sequence 2243, Application US/10276774

US-11-021-951-154

Query Match 99.3%; Score 1938.5; DB 20; Length 371;
Best Local Similarity 99.7%; Pred. No. 3.1e-164;
Matches 371; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNDYNTSLVENHLCPTATEGPLMASFKAVFVPVAYS 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNDYNTSLVENHLCPTATEGPLMASFKAVFVPVAYS 60

QY 61 IFLGVGNVNLVILRHRQTRSTETFLPHLAVADLLVFLPPFAVAGSGVWGLGTF 120
DB 61 IFLGVGNVNLVILRHRQTRSTETFLPHLAVADLLVFLPPFAVAGSGVWGLGTF 120

QY 121 LCKTVIALHKVNFYCSSILLACIAVDYLAIVHVAHYRHRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSILLACIAVDYLAIVHVAHYRHRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNLSRPTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILPAKVSQGHNNLSRPTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVRLROAQRPRQKAVRAIVLVTISFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
DB 241 -VVRLROAQRPRQKAVRAIVLVTISFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 299

QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFSPMRRSSL 360
DB 300 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFSPMRRSSL 359

QY 361 SESENATSLTTF 372
DB 360 SESENATSLTTF 371

RESULT 9
US-10-251-385-20
; Sequence 20, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-20

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

QY 11 LENLEDLFWELDRDLDNDYNTSLVENHLCPTATEGPLMASFKAVFVPVAYSLLIFLLGVGNV 70
DB 20 LENFSSSY---DYGENESD-SCTSPPCQ---DFSINFDRAFLPALYSLLFLGLGNG 72

QY 71 LVLVILRHRQTRSTETFLPHLAVADLLVFLPPFAVAGSGVWGLGTFCKTIALHK 130
DB 73 AVAALLSRRTALSSTDTFLLHLAVADTLVLTPLWADAAVQVWFGSLCKVAGALFN 132

QY 131 VNFYCSSILLACIAVDYLAIVHVAHYRHRLLSIHITCGTIWLVGFLALPEILFAKV 190
DB 131 VNFYCSSILLACIAVDYLAIVHVAHYRHRLLSIHITCGTIWLVGFLALPEILFAKV 190

DB 133 INFAGALLLACISFDRLYNIVHATQLYRRGPPARVTLTCLAVMGLCLLFLPDPFIFL-- 190
QY 191 SQGHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYGVVHRLROA 248
DB 191 -SAHDERLNATHCOYNFQVGR---ALRVQLVAGFLLPMLVMAYCYAHILAVL-LV 244
QY 249 QRRPQKAVRAIVLVTISFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSLPVAITMCE 308
DB 245 SRGQRLRAMLVVVVVAFALCWTPTVHLVLDLMDLALARNCGRESRVDVAKSVTS 304
QY 309 FLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFSPMRR--SSLSESENAT 367
DB 305 GLGYWHCCCLNPLLYAFVGKFRERMMWMLLLRLGCPNQRGLQRPSSRRDSSWSETSEAS 364

RESULT 10
US-10-225-567A-74
; Sequence 74, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-74

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

QY 11 LENLEDLFWELDRDLDNDYNTSLVENHLCPTATEGPLMASFKAVFVPVAYSLLIFLLGVGNV 70
DB 20 LENFSSSY---DYGENESD-SCTSPPCQ---DFSINFDRAFLPALYSLLFLGLGNG 72

QY 71 LVLVILRHRQTRSTETFLPHLAVADLLVFLPPFAVAGSGVWGLGTFCKTIALHK 130
DB 73 AVAALLSRRTALSSTDTFLLHLAVADTLVLTPLWADAAVQVWFGSLCKVAGALFN 132

QY 131 VNFYCSSILLACIAVDYLAIVHVAHYRHRLLSIHITCGTIWLVGFLALPEILFAKV 190
DB 133 INFAGALLLACISFDRLYNIVHATQLYRRGPPARVTLTCLAVMGLCLLFLPDPFIFL-- 190
QY 191 SQGHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYGVVHRLROA 248
DB 191 -SAHDERLNATHCOYNFQVGR---ALRVQLVAGFLLPMLVMAYCYAHILAVL-LV 244
QY 249 QRRPQKAVRAIVLVTISFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSLPVAITMCE 308
DB 245 SRGQRLRAMLVVVVVAFALCWTPTVHLVLDLMDLALARNCGRESRVDVAKSVTS 304
QY 309 FLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFSPMRR--SSLSESENAT 367
DB 305 GLGYWHCCCLNPLLYAFVGKFRERMMWMLLLRLGCPNQRGLQRPSSRRDSSWSETSEAS 364

RESULT 11
US-10-345-680-59
; Sequence 59, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING 34021, 44099, 25278,
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 62553, 302, 323,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: ME102-012P1RNM_OMNI
CURRENT APPLICATION NUMBER: US/10/345,680
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/349,511
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/374,063
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/414,262
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 368
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-345-680-59

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
QY 11 LENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVPVAYSILIFLLGVIGNV 70
Db 20 LENFSSSY---DYGENESD--SCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLLGLLNG 72
QY 71 LVLVILHRHQTRSTSTFELHLAVADLLVFLPFAVAGSGVGVGLTFLCKTVIALHK 130
Db 73 AVAAVLLSRRTALSSDTDFELHLAVADTLVLTLPLWADAAVQWVFGSLCKVAGALFN 132
QY 131 VNFYCSLLACIAVDRLYLAIHVAVHYRHRRLLSIHITCGTIWLVGFLALPEILFAKV 190
Db 133 INFYAGALLACISFDRLYINIVHATQLYRRGPPARVTLTCLAVMGLCLLFPALPDFL-- 190
QY 191 SOGHNNSL--PRCTSEQENQAETHAWFTSRFLYHVAGFLPMLVMGVCYGVVHRLROA 248
Db 245 SRGQRRLRANRLVVVVVAFALCWTPTPHLVLVVDILMDLGALARNCGRESRVDVAKSVTS 304
QY 309 FLGLAHCCLNPMLYTFAGVFKPRSDLSRLTLKLGCTGPASLCQLFPFSWR--SSLSESENAT 367
Db 305 GLGYMHCCLNPLLYAFVGVKFRERWMLLLRLGCPNQRGLQRPSSRRDSSWSETSEAS 364

RESULT 12
US-10-251-686-2
Sequence 2, Application US/10251686
Publication No. US20030158392A1
GENERAL INFORMATION:
APPLICANT: Loetscher, Marcel
Moser, Bernhard
Qin, Shixin
Mackay, Charles R.

TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/251,686
FILING DATE: 20-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI96-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-251-686-2

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
QY 11 LENLEDLFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVPVAYSILIFLLGVIGNV 70
Db 20 LENFSSSY---DYGENESD--SCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLLGLLNG 72
QY 71 LVLVILHRHQTRSTSTFELHLAVADLLVFLPFAVAGSGVGVGLTFLCKTVIALHK 130
Db 73 AVAAVLLSRRTALSSDTDFELHLAVADTLVLTLPLWADAAVQWVFGSLCKVAGALFN 132
QY 131 VNFYCSLLACIAVDRLYLAIHVAVHYRHRRLLSIHITCGTIWLVGFLALPEILFAKV 190
Db 133 INFYAGALLACISFDRLYINIVHATQLYRRGPPARVTLTCLAVMGLCLLFPALPDFL-- 190
QY 191 SOGHNNSL--PRCTSEQENQAETHAWFTSRFLYHVAGFLPMLVMGVCYGVVHRLROA 248
Db 191 -SAHDERLNATHCQYNFPQVGR-----ALRVQLVAGFLPMLVMAYCYAHILAVL-LV 244
QY 249 QRRPQOKAVRVAIVLTSIFFLCWSPHYIVIFDLTLARLKAVDNTCKLNGSLPVAITMCE 308
Db 245 SRGQRRLRANRLVVVVVAFALCWTPTPHLVLVVDILMDLGALARNCGRESRVDVAKSVTS 304
QY 309 FLGLAHCCLNPMLYTFAGVFKPRSDLSRLTLKLGCTGPASLCQLFPFSWR--SSLSESENAT 367
Db 305 GLGYMHCCLNPLLYAFVGVKFRERWMLLLRLGCPNQRGLQRPSSRRDSSWSETSEAS 364

RESULT 13
US-10-239-423-78
Sequence 78, Application US/10239423
Publication No. US2003018689A1

```
; GENERAL INFORMATION:
; APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 78
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-78

Query Match          32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

QY 11 LENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFVPVAYSLIFLLGVGNV 70
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 LENFSSSY---DYGENESD-SCTSPPCQ---DPSLNFDRAPFLPALYSLFLLGLLGGNG 72
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 LVLVILERHQRTRSSSTETFLHLAVADTLVLTPFWAAGVGVGLTFLCKTVIALHK 130
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 AVAAVLLSRRTALSSDTDFLLHLAVADTLVLTPFWAAGVGVGLTFLCKTVIALHK 132
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 VNPYCSLLACIADRYLAIVHAYHRRRLSLTHITGCTIWLGVGLLALPEILFAKV 248
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 INFYAGALLLACISFDRIYINIVHATQLYRRGPPARVTLTCLAVWGLCLLFPALPDI 190
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 191 SQGHNNSL--PRCTFSQENQAETHAWFTSRFLYHVGFLPMLVGMWCVGVVHRLQA 248
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 -SAHDERLNATHCQYNFPQVGR-----ALRVQLVAGFLPMLVGMWCVGVVHRLQA 244
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 QRRPQKAVRAVAILVTSIFFLCWSPYHIVFLDTLRLKAVDNTCKLNGSLPVAITMCE 308
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 SRGQRLRAMRLVVVVVAFALCWTPYHLVLDLMDLGALARNCGRESRDVAKSVTS 304
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 FLGLAHCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRR-SSLSESENAT 367
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 GLGYNHCCLNPLLYAFVGVKFRERMMWMLLLRLGCPNQRGLQRPSSRRDSSWSETSEAS 364
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-10-411-284-4
; Sequence 4, Application US/10411284
; Publication No. US2003022426A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
; FILE REFERENCE: PF218P1
; CURRENT APPLICATION NUMBER: US/10/411,284
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,725
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/101,518
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: PCT/US96/00499
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in Ver. 3.1
; SEQ ID NO 4
; LENGTH: 368
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-284-4

Query Match          32.5%; Score 635; DB 15; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

QY 11 LENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFVPVAYSLIFLLGVGNV 70
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 LENFSSSY---DYGENESD-SCTSPPCQ---DPSLNFDRAPFLPALYSLFLLGLLGGNG 72
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 LVLVILERHQRTRSSSTETFLHLAVADTLVLTPFWAAGVGVGLTFLCKTVIALHK 130
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 AVAAVLLSRRTALSSDTDFLLHLAVADTLVLTPFWAAGVGVGLTFLCKTVIALHK 132
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 VNPYCSLLACIADRYLAIVHAYHRRRLSLTHITGCTIWLGVGLLALPEILFAKV 190
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 INFYAGALLLACISFDRIYINIVHATQLYRRGPPARVTLTCLAVWGLCLLFPALPDI 190
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 191 SQGHNNSL--PRCTFSQENQAETHAWFTSRFLYHVGFLPMLVGMWCVGVVHRLQA 248
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 -SAHDERLNATHCQYNFPQVGR-----ALRVQLVAGFLPMLVGMWCVGVVHRLQA 244
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 QRRPQKAVRAVAILVTSIFFLCWSPYHIVFLDTLRLKAVDNTCKLNGSLPVAITMCE 308
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 SRGQRLRAMRLVVVVVAFALCWTPYHLVLDLMDLGALARNCGRESRDVAKSVTS 304
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 FLGLAHCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRR-SSLSESENAT 367
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 GLGYNHCCLNPLLYAFVGVKFRERMMWMLLLRLGCPNQRGLQRPSSRRDSSWSETSEAS 364
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-10-295-027-752
; Sequence 752, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 752

; LENGTH: 368

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; TYPE: PRT

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ORGANISM: Homo sapiens

US-10-295-027-752

[illegible]

Search completed: August 30, 2005, 00:01:24
Job time : 166 secs